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(54) **MODIFIED HUMAN PLASMA POLYPEPTIDE
OR FC SCAFFOLDS AND THEIR USES**

(75) Inventors: **Joseph Sheffer**, Cardiff, CA (US); **Thea Norman**, San Diego, CA (US); **Richard D. Dimarchi**, Carmel, IN (US); **Anna-Maria A. Hays Putnam**, San Diego, CA (US); **Feng Tian**, San Diego, CA (US); **Stephanie Chu**, Simi Valley, CA (US); **Denise Krawitz**, Novato, CA (US); **Ho Sung Cho**, San Diego, CA (US)

(73) Assignee: **Ambrex, Inc.**, La Jolla, CA (US)

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Related U.S. Application Data

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(60) Provisional application No. 60/843,215, filed on Sep. 8, 2006, provisional application No. 60/928,485, filed on May 8, 2007.

(51) **Int. Cl.**

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(52) **U.S. Cl.**

CPC **C07K 14/47** (2013.01); **C07K 19/00** (2013.01); **C07K 2319/00** (2013.01); **A61K 38/00** (2013.01); **C07K 14/765** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

(56)

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Primary Examiner — Bridget E Bunner

Assistant Examiner — Fozia Hamud

(74) *Attorney, Agent, or Firm* — John W. Wallen, III; Kristin S. Eaton

(57)

ABSTRACT

Modified human plasma polypeptides or Fc and uses thereof are provided.

4 Claims, 18 Drawing Sheets

Figure 1

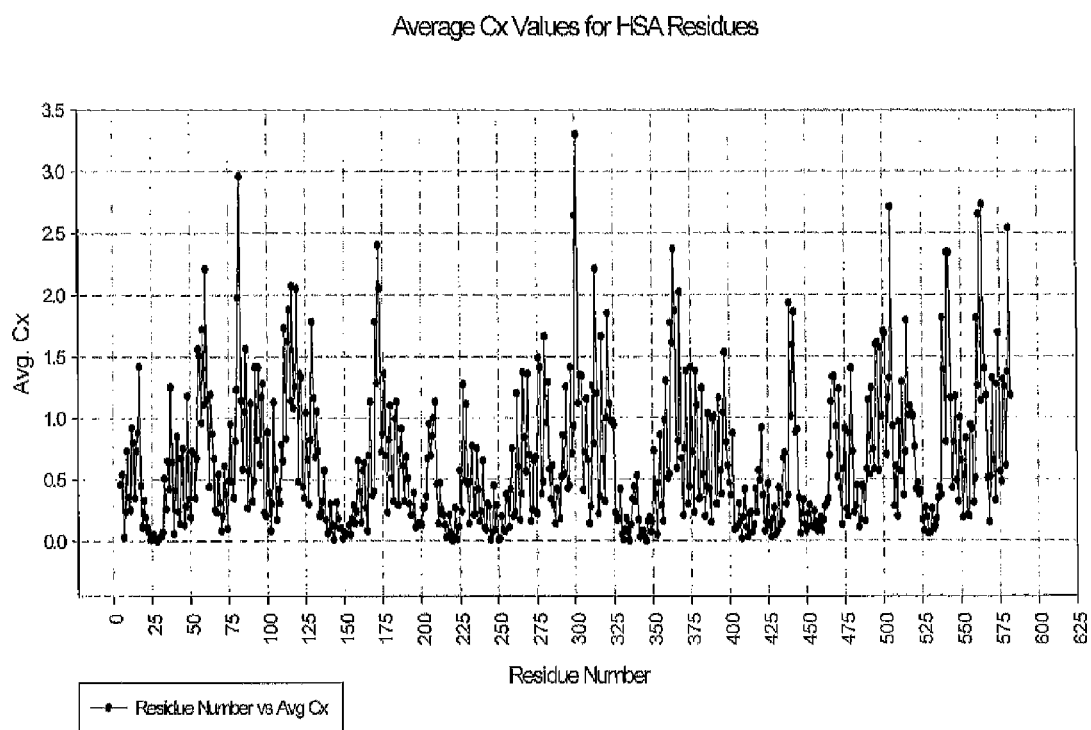


Figure 2

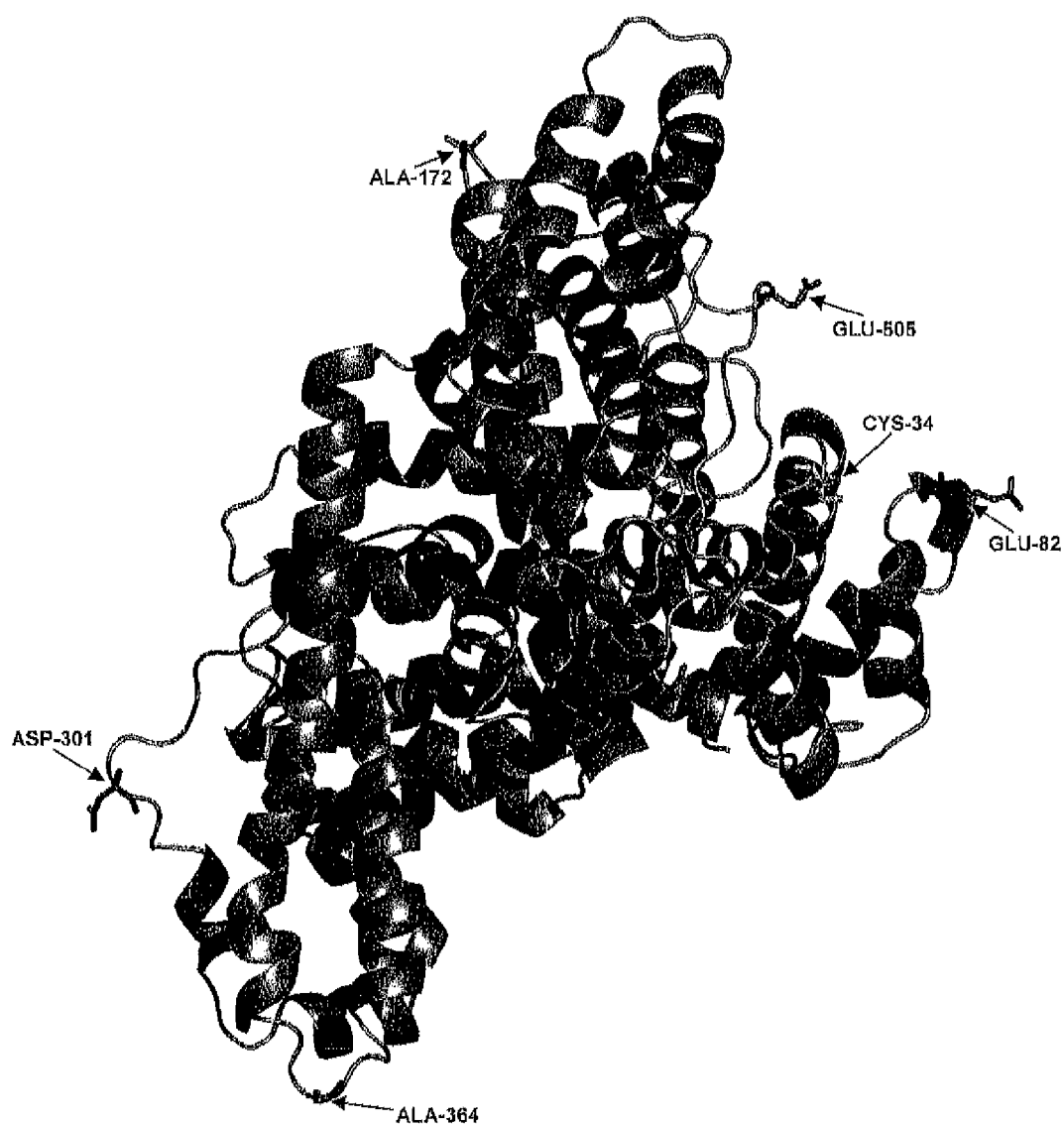


Figure 3

Group I	Residue #	Cx value	Group II	Residue #	Cx value	Group III	Residue #	Cx value
ASP	301	3.3	ARG	81	1.98	GLU	280	1.66
GLU	82	2.96	LYS	439	1.93	LYS	317	1.66
LYS	564	2.73	ARG	114	1.88	ALA	363	1.61
GLU	505	2.71	ASP	365	1.87	THR	496	1.61
ASP	562	2.65	GLU	442	1.86	GLU	495	1.59
ALA	300	2.64	GLU	321	1.85	VAL	498	1.57
ALA	581	2.54	LYS	538	1.81	ALA	55	1.56
ALA	172	2.4	LYS	560	1.81	GLU	86	1.56
ALA	364	2.37	THR	515	1.79	GLN	397	1.53
LYS	541	2.34	ASP	129	1.78	ASP	56	1.51
GLU	542	2.34	GLN	170	1.78	LYS	276	1.49
GLU	60	2.21	ALA	362	1.77	GLU	17	1.42
LYS	313	2.21	ASN	111	1.73	ALA	92	1.41
VAL	116	2.07	SER	58	1.72	GLN	94	1.41
GLU	119	2.05	LYS	500	1.7	GLU	277	1.41
ASP	173	2.05	LYS	574	1.69	GLU	297	1.41
GLU	368	2.02	GLU	501	1.68	ASP	375	1.41

Figure 4

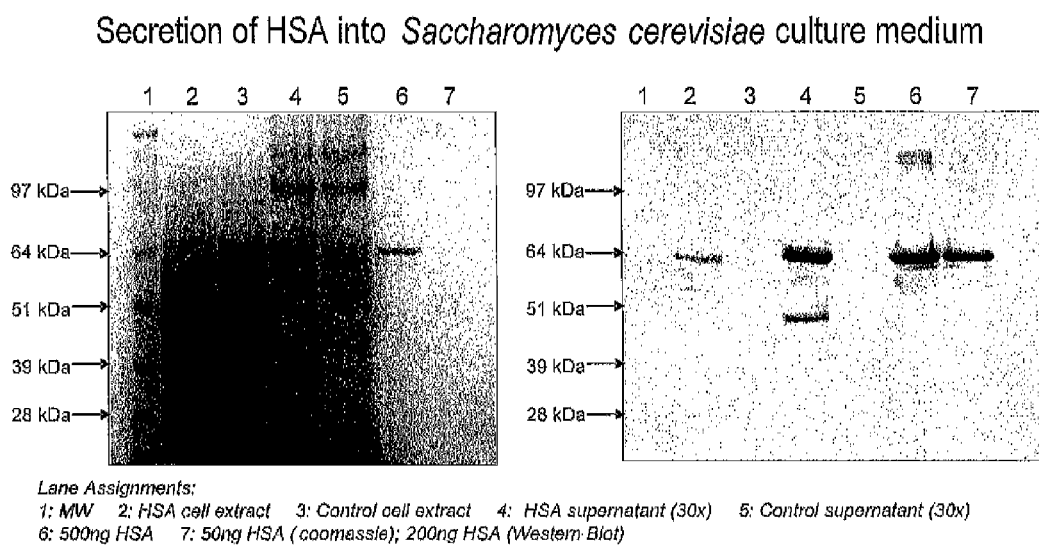
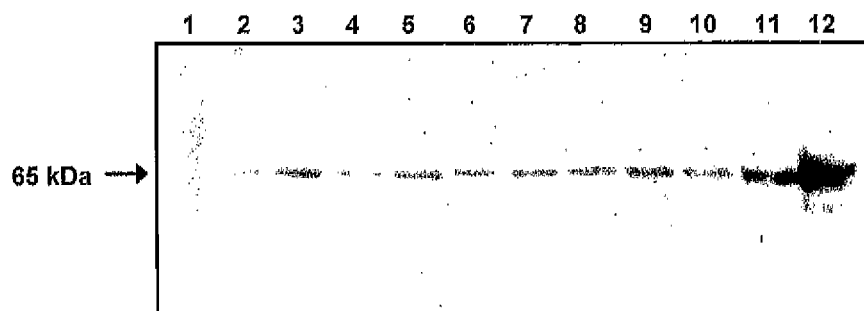


Figure 5**Detection of suppressed HSA by Western Blot****Lane Assignments:**

- 1: MW
- 2: pGADHSA(C34Amb)
- 3: pGADHSA(C34Amb) + *E. coli* TyrRS, tRNA_{CUA}
- 4: pGADHSA(C34Amb) + *E. coli* pAFRS/tRNA_{CUA}
- 5: pGADHSA(C34Amb) + *E. coli* pAFRS/tRNA_{CUA} + 1mM pAF
- 6: pGADHSA(C34Amb) + *E. coli* pAzRS/tRNA_{CUA}
- 7: pGADHSA(C34Amb) + *E. coli* pAzRS/tRNA_{CUA} + 1mM AzF
- 8: pGADHSA(C34Amb) + *E. coli* pBzRS/tRNA_{CUA}
- 9: pGADHSA(C34Amb) + *E. coli* pBzRS/tRNA_{CUA} + 1mM BzF
- 10: pGADHSA(C34Amb) + *E. coli* pOMeRS/tRNA_{CUA}
- 11: pGADHSA(C34Amb) + *E. coli* pOMeRS/tRNA_{CUA} + 1mM OMeF
- 12: 500 ng HSA control

Figure 6

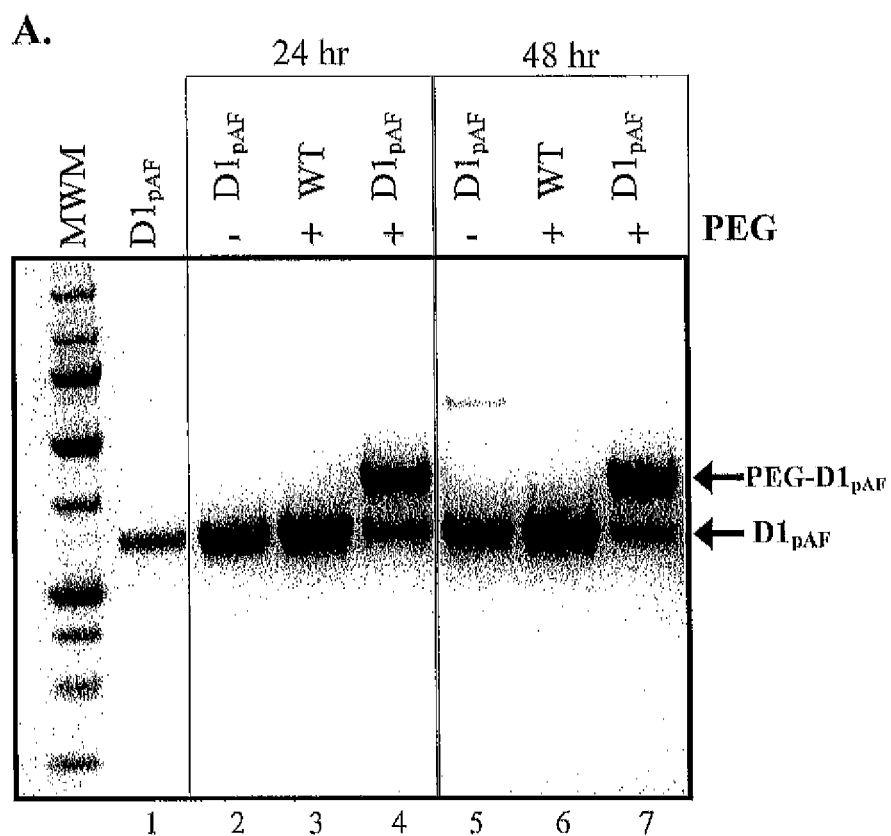


Figure 6

B.

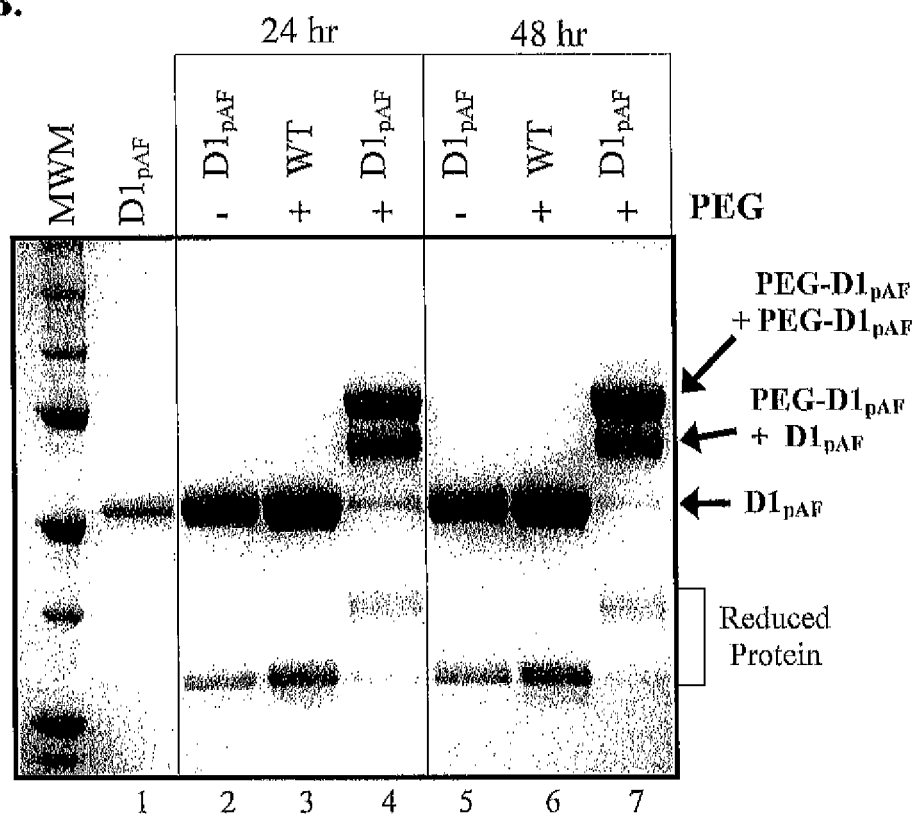


Figure 7A

WT Fc Nucleotide sequence:

ATGTACAGGATGCAACTCCTGTCTTGCACTTAAGTCTTGCACTTGTACGAATTCGGACA
AAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTT
CCCCC AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTG
GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA
ATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCAC
CGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC
CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACA
CCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG
CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATAAG
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCA
CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

(SEQ ID NO: 20)

Figure 7B**Fc Protein Sequence:**

Signal Sequence - completely absent in purified protein
(underlined)

Mature Protein: wt has D at position 1
Suppressed protein has pAF at position 1
(marked with an asterisk)

*

MYRMQLLSCI ALSLALVTNS DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVHL QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK-

(SEQ ID NO: 21)

Figure 7C

Mature Fc Protein Sequence:

Mature Protein: wt has D at position 1
Suppressed protein has pAF at position 1
(marked with an asterisk)

*

DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTIVLH QDWLNGKEYK
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK
GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL TVDKSRWQQG
NVFSCSV MHE ALHNHYTQKS LSLSPGK

(SEQ ID NO: 22)

Figure 7D**Fc Nucleotide sequence without signal sequence:**

GACAAAAC TCACACATGCCACCGTGCC CAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC
TCTTCCCCC AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGT
GGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG
CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTG
TACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC TA
CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACA
ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

(SEQ ID NO: 23)

Figure 8A

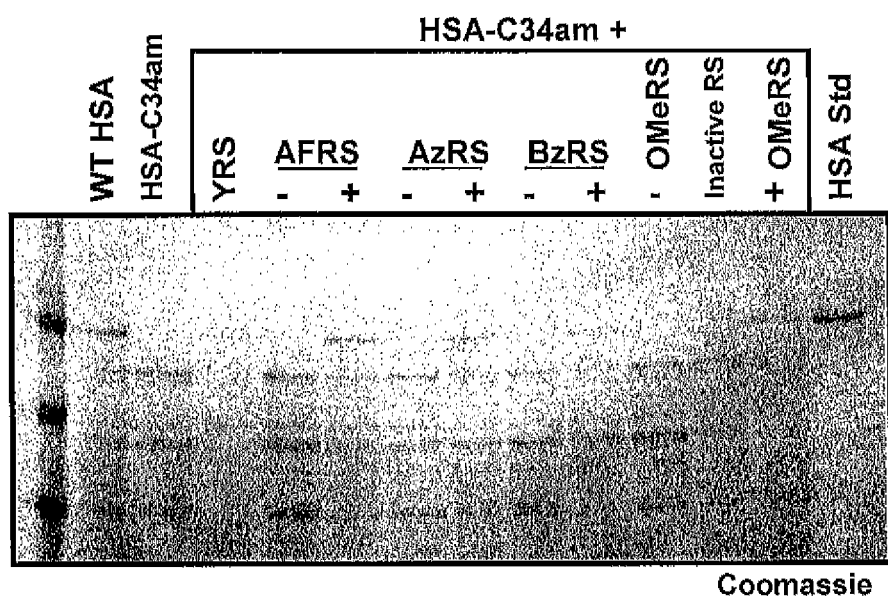
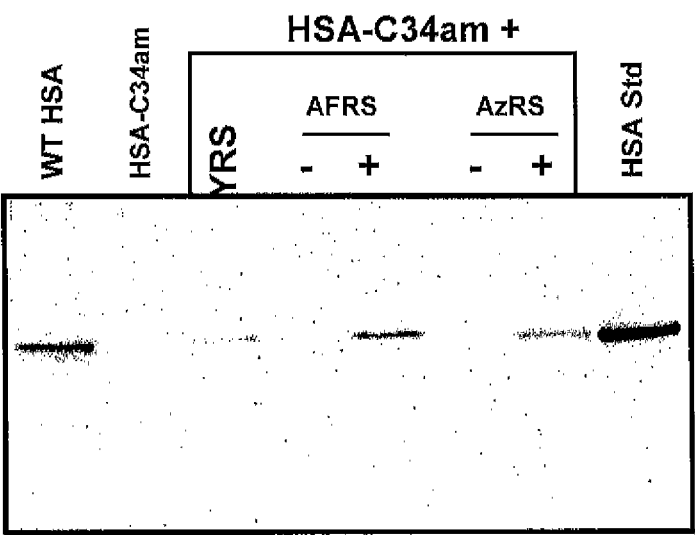
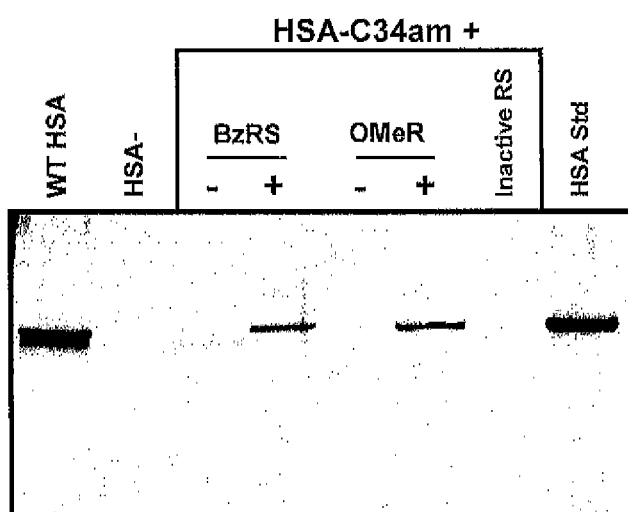


Figure 8B



α -HSA Western

Figure 8C



α -HSA Western

Figure 9

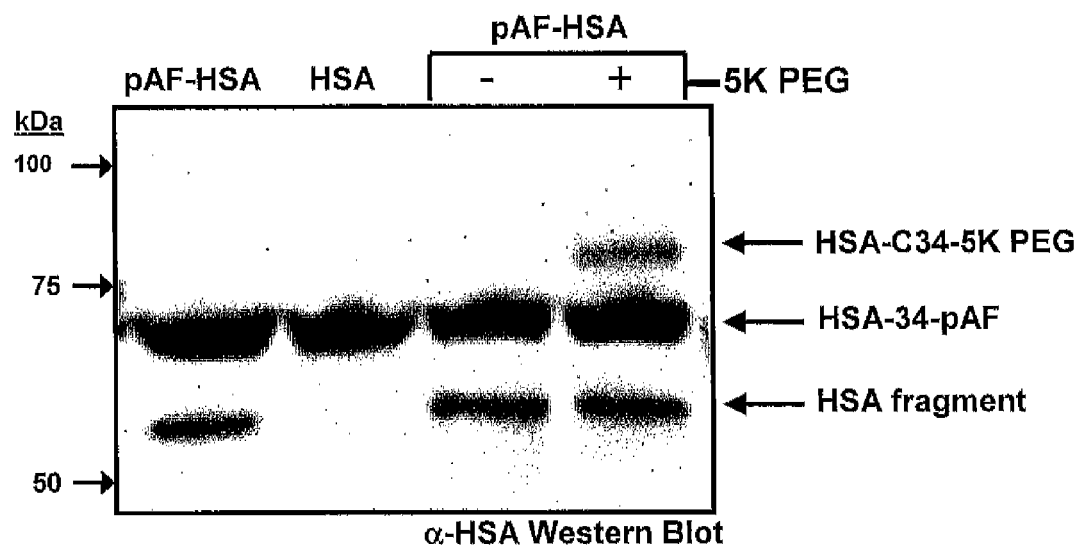


Figure 10

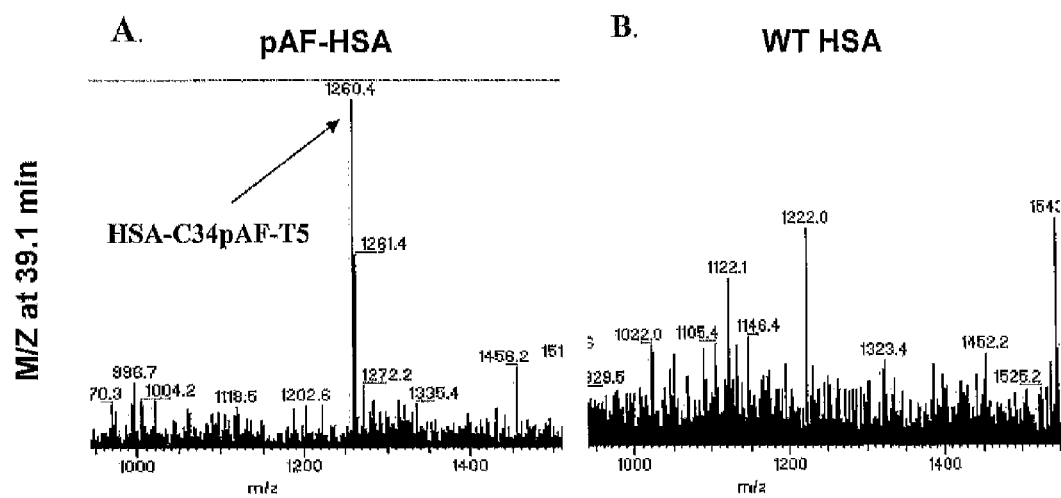


Figure 11A

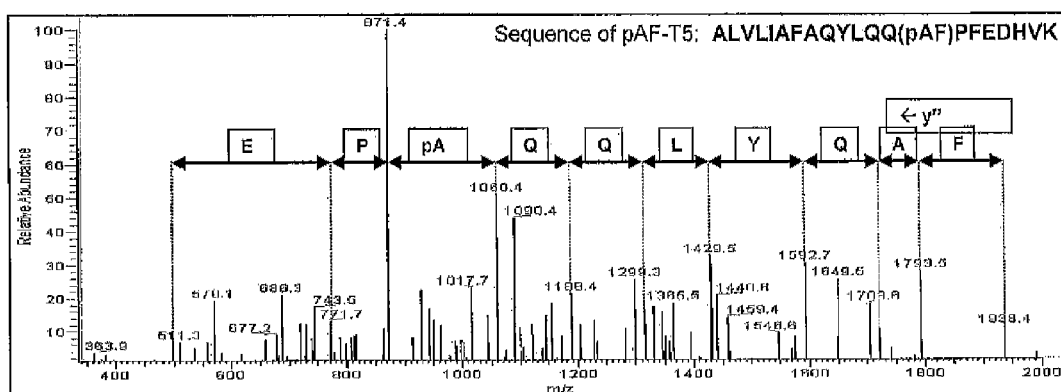


Figure 11B

b	Amino Acid	y"
72.05	Ala	x
185.13	Leu	2412.22
284.20	Val	2335.13
397.28	Leu	2236.06
510.37	Ile	2122.98
581.40	Ala	2009.90
728.47	Phe	1938.86
799.51	Ala	1791.80
927.57	Gln	1720.76
1090.63	Tyr	1592.70
1203.71	Leu	1429.63
1331.77	Gln	1316.55
1459.83	Gln	1188.49
1648.83	pAF	1060.43
1745.88	Pro	871.43
1892.95	Phe	774.38
2022.00	Glu	627.31
2137.02	As	498.27
2274.08	His	383.24
2873.15	Val	246.18
x	Lys	147.11

Predicted ion masses

Identified ions in Figure 13A

Identified ions (not shown)

MODIFIED HUMAN PLASMA POLYPEPTIDE OR FC SCAFFOLDS AND THEIR USES

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 11/927,247 filed on Oct. 29, 2007, which is a continuation of International Patent Application No. PCT/US2007/019528 filed on Sep. 7, 2007, which is incorporated by reference herein in its entirety and claims the benefit of priority to U.S. provisional patent application 60/843,215 filed Sep. 8, 2006, and U.S. provisional patent application 60/928,485 filed May 8, 2007, the specifications and disclosures of which are incorporated herein in their entirety for all purposes.

FIELD OF THE INVENTION

This invention relates to human plasma polypeptides or Fc molecules modified to comprise at least one non-naturally-encoded amino acid.

BACKGROUND OF THE INVENTION

Human blood plasma is comprised of a variety of proteins that carry out a variety of functions. The protein components of blood plasma are a focus of intense research. See, for example, Anderson et al., *Molecular & Cellular Proteomics*, 3.4:311-326 (2004); and Ping et al., *Proteomics*, 5:3506-3519 (2005) for a description of the known protein components of human blood plasma. The most common protein found in human blood plasma is albumin.

Human albumin, also referred to as serum albumin, is a multifunctional protein found in blood plasma. It is an important factor in the regulation of plasma volume and tissue fluid balance through its contribution to the colloid osmotic pressure of plasma. Albumin also functions as a carrier for other molecules found in the bloodstream. Albumin normally constitutes 50-60% of plasma proteins and because of its relatively low molecular weight (66,500 Daltons), exerts 80-85% of the colloidal osmotic pressure of the blood. Albumin regulates transvascular fluid flux and hence, intra and extravascular fluid volumes, and transports lipid and lipid-soluble substances. Albumin solutions are frequently used for plasma volume expansion and maintenance of cardiac output in the treatment of certain types of shock or impending shock including those resulting from burns, surgery, hemorrhage, or other trauma or conditions in which a circulatory volume deficit is present.

Albumin has a blood circulation half-life of approximately two weeks and is designed by nature to carry other molecules such as lipids, peptides, and other proteins. A hydrophobic binding pocket and a free thiol cysteine residue (Cys34) are features that enable this function. Due to its low pKa (approx. 7) Cys34 is one of the more reactive thiol groups appearing in human plasma. The Cys34 of albumin also accounts for the major fraction of thiol concentration in blood plasma (over 80%) (Kratz et al., *J. Med. Chem.*, 45(25):5523-33 (2002)). The ability of albumin through its reactive thiol to act as a carrier has been utilized for therapeutic purposes. For example, attachment of drugs to albumin to improve the pharmacological properties of the drugs has been described (Kremer et al., *Anticancer Drugs*, 13(6):615-23 (2002); Kratz et al., *J. Drug Target.*, 8(5):305-18 (2000); Kratz et al., *J. Med. Chem.*, 45(25):5523-33 (2002); Tanaka et al., *Bioconjug. Chem.*, 2(4):26-9 (1991); Dosio et al., *J. Control. Release*, 76(1-2):107-17 (2001); Dings et al., *Cancer Lett.*, 194(1):55-

66 (2003); Wunder et al., *J. Immunol.*, 170(9):4793-801 (2003); Christie et al., *Biochem. Pharmacol.*, 36(20):3379-85 (1987)). The attachment of peptide and protein therapeutics to albumin has also been described (Holmes et al., *Bioconjug. Chem.*, 11 (4):439-44 (2000); Leger et al., *Bioorg. Med. Chem. Lett.*, 13(20):3571-5 (2003); Paige et al., *Pharm. Res.*, 12(12):1883-8 (1995)). Conjugates of albumin and interferon-alpha (Albuferon™) and of albumin and human growth hormone (Albutropin™) and of albumin and interleukin-2 (Albuleukin™) have also been made. The art also describes the use of standard recombinant molecular biology techniques to generate an albumin-protein fusion (U.S. Pat. No. 6,548,653, which is incorporated by reference herein). All but the latter conjugates with albumin involve ex vivo conjugate formation with an exogenous albumin. Potential drawbacks to using exogenous sources of albumin are contamination or an immunogenic response.

In vivo attachment of therapeutic agents to albumin has also been described, where, for example, a selected peptide is modified prior to administration to allow albumin to bind to the peptide. This approach is described using dipeptidyl peptidase IV-resistant glucagon-like-peptide-1 (GLP-1) analogs (Kim et al., *Diabetes*, 52(3):75'-9 (2003)). A specific linker ([2-[2-[2-maleimido-propionamido-(ethoxy)-ethoxy]-acetamide) was attached to an added carboxyl-terminal lysine on the peptide to enable a cysteine residue of albumin to bind with the peptide. Others have investigated attaching specific tags to peptides or proteins in order to increase their binding to albumin in vivo (Koehler et al., *Bioorg Med. Chem. Lett.*, 12(20):2883-6 (2002); Dennis et al., *J. Biol. Chem.*, 277(38):35035-35043 (2002)); Smith et al., *Bioconjug. Chem.*, 12:750-756 (2001)). A similar approach has been used with small molecule drugs, where a derivative of the drug was designed specifically to have the ability to bind with a cysteine residue of albumin. For example, this pro-drug strategy has been used for doxorubicin derivatives where the doxorubicin derivative is bound to endogenous albumin at its cysteine residue at position 34 (Cys34; Kratz et al., *J. Med. Chem.*, 45(25): 5523-33 (2002)). The in vivo attachment of a therapeutic agent to albumin has the advantage, relative to the ex vivo approach described above, in that endogenous albumin is used, thus obviating problems associated with contamination or an immunogenic response to the exogenous albumin. Yet, the prior art approach of in vivo formation of drug conjugates with endogenous albumin involves a permanent covalent linkage between the drug and the albumin. To the extent the linkage is cleavable or reversible, the drug or peptide released from the conjugate is in a modified form of the original compound.

Human serum albumin has been expressed in yeast host cells including *Saccharomyces cerevisiae* (Etcheverry et al., (1986) *BioTechnology* 8:726, and EPA 123 544), *Pichia pastoris* (EPA 344 459), and *Kluyveromyces* (Fleer et al., (1991) *BioTechnology* 9:968-975), and in *E. coli* (Latta et al., (1987) *BioTechnology* 5:1309-1314), which are incorporated by reference herein.

A naturally produced antibody (Ab) is a tetrameric structure consisting of two identical immunoglobulin (Ig) heavy chains and two identical light chains. Immunoglobulins are molecules containing polypeptide chains held together by disulfide bonds, typically having two light chains and two heavy chains. In each chain, one domain (V) has a variable amino acid sequence depending on the antibody specificity of the molecule. The other domains (C) have a rather constant sequence common to molecules of the same class.

The heavy and light chains of an Ab consist of different domains Each light chain has one variable domain (VL) and

one constant domain (CL), while each heavy chain has one variable domain (VH) and three or four constant domains (CH). Each domain, consisting of about 110 amino acid residues, is folded into a characteristic β -sandwich structure formed from two β -sheets packed against each other, the immunoglobulin fold. The VL domains each have three complementarity determining regions (CDR1-3) and the VH domains each have up to four complementarity determining regions (CDR1-4), that are loops, or turns, connecting β -strands at one end of the domains. The variable regions of both the light and heavy chains generally contribute to antigen specificity, although the contribution of the individual chains to specificity is not necessarily equal. Antibody molecules have evolved to bind to a large number of molecules by using randomized CDR loops.

Functional substructures of Abs can be prepared by proteolysis and by recombinant methods. They include the Fab fragment, which comprises the VH-CH1 domains of the heavy chain and the VL-CH1 domains of the light chain joined by a single interchain disulfide bond, and the Fv fragment, which comprises only the VH and VL domains, and the Fc portion which comprises the non-antigen binding region of the molecule. In some cases, a single VH domain retains significant affinity for antigen (Ward et al., 1989, Nature 341, 554-546). It has also been shown that a certain monomeric κ light chain will specifically bind to its antigen. (L. Masat et al., 1994, PNAS 91:893-896). Separated light or heavy chains have sometimes been found to retain some antigen-binding activity as well (Ward et al., 1989, Nature 341, 554-546).

Another functional substructure is a single chain Fv (scFv), comprised of the variable regions of the immunoglobulin heavy and light chain, covalently connected by a peptide linker (S-z Hu et al., 1996, Cancer Research, 56, 3055-3061). These small (Mr 25,000) proteins generally retain specificity and affinity for antigen in a single polypeptide and can provide a convenient building block for larger, antigen-specific molecules. The short half-life of scFvs in the circulation limits their therapeutic utility in many cases.

A small protein scaffold called a "minibody" was designed using a part of the Ig VH domain as the template (Pessi et al., 1993, Nature 362, 367-369). Minibodies with high affinity (dissociation constant (K_d) about 10^{-7} M) to interleukin-6 were identified by randomizing loops corresponding to CDR1 and CDR2 of VH and then selecting mutants using the phage display method (Martin et al., 1994, EMBO J. 13, 5303-5309).

Camels often lack variable light chain domains when IgG-like material from their serum is analyzed, suggesting that sufficient antibody specificity and affinity can be derived from VH domains (three or four CDR loops) alone. "Camelized" VH domains with high affinity have been made, and high specificity can be generated by randomizing only the CDR3.

An alternative to the "minibody" is the "diabody." Diabodies are small bivalent and bispecific antibody fragments, having two antigen-binding sites. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) on the same polypeptide chain (V_H - V_L). Diabodies are similar in size to the Fab fragment. By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. These dimeric antibody fragments, or "diabodies," are bivalent and bispecific. See, P. Holliger et al., PNAS 90:6444-6448 (1993).

An antibody fragment includes any form of an antibody other than the full-length form. Antibody fragments herein

include antibodies that are smaller components that exist within full-length antibodies, and antibodies that have been engineered. Antibody fragments include but are not limited to Fv, Fc, Fab, and (Fab')₂, single chain Fv (scFv), diabodies, triabodies, tetrabodies, bifunctional hybrid antibodies, CDR1, CDR2, CDR3, combinations of CDR's, variable regions, framework regions, constant regions, and the like (Maynard & Georgiou, 2000, Annu. Rev. Biomed. Eng. 2:339-76; Hudson, 1998, Curr. Opin. Biotechnol. 9:395-402).

CDR peptides and organic CDR mimetics have been made (Dougall et al., 1994, Trends Biotechnol. 12, 372-379). CDR peptides are short, typically cyclic, peptides which correspond to the amino acid sequences of CDR loops of antibodies. CDR loops are responsible for antibody-antigen interactions. CDR peptides and organic CDR mimetics have been shown to retain some binding affinity (Smyth & von Itzstein, 1994, J. Am. Chem. Soc. 116, 2725-2733). Mouse CDRs have been grafted onto the human Ig framework without the loss of affinity (Jones et al., 1986, Nature 321, 522-525; Riechmann et al., 1988).

In the body, specific Abs are selected and amplified from a large library (affinity maturation). The processes can be reproduced in vitro using combinatorial library technologies. The successful display of Ab fragments on the surface of bacteriophage has made it possible to generate and screen a vast number of CDR mutations (McCafferty et al., 1990, Nature 348, 552-554; Barbas et al., 1991, Proc. Natl. Acad. Sci. USA 88, 7978-7982; Winter et al., 1994, Annu. Rev. Immunol. 12, 433-455). An increasing number of Fabs and Fvs (and their derivatives) are produced by this technique. The combinatorial technique can be combined with Ab mimics.

A number of protein domains that could potentially serve as protein scaffolds have been expressed as fusions with phage capsid proteins. Review in Clarkson & Wells, Trends Biotechnol. 12:173-184 (1994). Several of these protein domains have already been used as scaffolds for displaying random peptide sequences, including bovine pancreatic trypsin inhibitor (Roberts et al., PNAS 89:2429-2433 (1992)), human growth hormone (Lowman et al., Biochemistry 30:10832-10838 (1991)), Venturini et al., Protein Peptide Letters 1:70-75 (1994)), and the IgG binding domain of *Streptococcus* (O'Neil et al., Techniques in Protein Chemistry V (Crabb, L., ed.) pp. 517-524, Academic Press, San Diego (1994)). These scaffolds have displayed a single randomized loop or region. Tendamisat has been used as a presentation scaffold on the filamentous phage M13 (McConnell and Hoess, 1995, J. Mol. Biol. 250:460-470).

The Fc portion of an immunoglobulin, includes but is not limited to, an antibody fragment which is obtained by removing the two antigen binding regions (the Fab fragments) from the antibody. One way to remove the Fab fragments is to digest the immunoglobulin with papain protease. Thus, the Fc portion is formed from approximately equal sized fragments of the constant region from both heavy chains, which associate through non-covalent interactions and disulfide bonds. The Fc portion can include the hinge regions and extend through the CH2 and CH3 domains to the C-terminus of the antibody. Representative hinge regions for human and mouse immunoglobulins can be found in Antibody Engineering, A Practical Guide, Borrebaeck, C. A. K., ed., W. H. Freeman and Co., 1992, the teachings of which are herein incorporated by reference. The Fc portion can further include one or more glycosylation sites. The amino acid sequences of numerous

representative Fc proteins containing a hinge region, CH2 and CH3 domains, and one N-glycosylation site are well known in the art.

There are five types of human immunoglobulin Fc regions with different effector functions and pharmacokinetic properties: IgG, IgA, IgM, IgD, and IgE. IgG is the most abundant immunoglobulin in serum. IgG also has the longest half-life in serum of any immunoglobulin (23 days). Unlike other immunoglobulins, IgG is efficiently recirculated following binding to an Fc receptor. There are four IgG subclasses G1, G2, G3, and G4, each of which has different effector functions. G1, G2, and G3 can bind C1q and fix complement while G4 cannot. Even though G3 is able to bind C1q more efficiently than G1, G1 is more effective at mediating complement-directed cell lysis. G2 fixes complement very inefficiently. The C1q binding site in IgG is located at the carboxy terminal region of the CH2 domain.

All IgG subclasses are capable of binding to Fc receptors (CD16, CD32, CD64) with G1 and G3 being more effective than G2 and G4. The Fc receptor binding region of IgG is formed by residues located in both the hinge and the carboxy terminal regions of the CH2 domain.

IgA can exist both in a monomeric and dimeric form held together by a J-chain. IgA is the second most abundant Ig in serum, but it has a half-life of only 6 days. IgA has three effector functions. It binds to an IgA specific receptor on macrophages and eosinophils, which drives phagocytosis and degranulation, respectively. It can also fix complement via an unknown alternative pathway.

IgM is expressed as either a pentamer or a hexamer, both of which are held together by a J-chain. IgM has a serum half-life of 5 days. It binds weakly to C1q via a binding site located in its CH3 domain. IgD has a half-life of 3 days in serum. It is unclear what effector functions are attributable to this Ig. IgE is a monomeric Ig and has a serum half-life of 2.5 days. IgE binds to two Fc receptors which drives degranulation and results in the release of proinflammatory agents.

Polypeptides of the present invention may contain any of the isotypes described above or may contain mutated Fc regions wherein the complement and/or Fc receptor binding functions have been altered, modified, or removed. Polypeptides of the present invention may contain any of the isotypes described above or may contain mutated Fc regions wherein the effector function has been altered, modified, or removed. Thus, the polypeptides of the present invention may contain the entire Fc portion of an immunoglobulin, fragments of the Fc portion of an immunoglobulin, or analogs thereof.

Polypeptides of the present invention can consist of single chain proteins or as multi-chain polypeptides. Two or more Fc proteins can be produced such that they interact through disulfide bonds that naturally form between Fc regions. These multimers can be homogeneous with respect to a conjugated molecule or they may contain different conjugated molecules at the N-terminus of the Fc portion of the fusion protein.

A Fc or Fc-like region may serve to prolong the in vivo plasma half-life of a compound fused to it. Since the Fc region of IgG produced by proteolysis has the same in vivo half-life as the intact IgG molecule and Fab fragments are rapidly degraded, it is believed that the relevant sequence for prolonging half-life reside in the CH₂ and/or CH₃ domains. Further, it has been shown in the literature that the catabolic rates of IgG variants that do not bind the high-affinity Fc receptor or C1q are indistinguishable from the rate of clearance of the parent wild-type antibody, indicating that the catabolic site is distinct from the sites involved in Fc receptor or C1q binding. [Wawrzynczak et al., (1992) Molecular Immunology 29:221]. Site-directed mutagenesis studies using a murine

IgG1 Fc region suggested that the site of the IgG1 Fc region that controls the catabolic rate is located at the CH2-CH3 domain interface. Fc regions can be modified at the catabolic site to optimize the half-life of the fusion proteins. The Fc region used for the fusion proteins of the present invention may be derived from an IgG1 or an IgG4 Fc region, and may contain both the CH2 and CH3 regions including the hinge region.

Chimeric molecules comprising Fc and one or more other molecules including, but not limited to, a polypeptide may be generated. The chimeric molecule can contain specific regions or fragments of Fc and the other molecule(s). Any such fragments can be prepared from the proteins by standard biochemical methods, or by expressing a polynucleotide encoding the fragment. A polypeptide, or a fragment thereof, can be produced as a fusion protein comprising human serum albumin (HSA), Fc, or a portion thereof. Fusions may be created by fusion of a polypeptide with a) the Fc portion of an immunoglobulin; b) an analog of the Fc portion of an immunoglobulin; and c) fragments of the Fc portion of an immunoglobulin.

Recently, an entirely new technology in the protein sciences has been reported, which promises to overcome many of the limitations associated with site-specific modifications of proteins. Specifically, new components have been added to the protein biosynthetic machinery of the prokaryote *Escherichia coli* (*E. coli*) (e.g., L. Wang, et al., (2001), *Science* 292:498-500) and the eukaryote *Saccharomyces cerevisiae* (*S. cerevisiae*) (e.g., J. Chin et al., *Science* 301:964-7 (2003), Drabkin et al., (1996) *Mol. Cell. Biol.*, 16:907) and in mammalian cells (Sakamoto et al., (2002) *Nucleic Acids Res.* 30:4692), which has enabled the incorporation of non-genetically encoded amino acids to proteins in vivo. A number of new amino acids with novel chemical, physical or biological properties, including photoaffinity labels and photoisomerizable amino acids, photocrosslinking amino acids (see, e.g., Chin, J. W., et al. (2002) *Proc. Natl. Acad. Sci. U.S.A.* 99:11020-11024; and, Chin, J. W., et al., (2002) *J. Am. Chem. Soc.* 124:9026-9027), keto amino acids, heavy atom containing amino acids, and glycosylated amino acids have been incorporated efficiently and with high fidelity into proteins in *E. coli* and in yeast in response to the amber codon, TAG, using this methodology. See, e.g., J. W. Chin et al., (2002), *Journal of the American Chemical Society* 124:9026-9027; J. W. Chin, & P. G. Schultz, (2002), *ChemBioChem* 3(11):1135-1137; J. W. Chin, et al., (2002), *PNAS United States of America* 99:11020-11024; and, L. Wang, & P. G. Schultz, (2002), *Chem. Comm.*, 1:1-11. All references are incorporated by reference in their entirety. These studies have demonstrated that it is possible to selectively and routinely introduce chemical functional groups, such as ketone groups, alkyne groups and azide moieties, that are not found in proteins, that are chemically inert to all of the functional groups found in the 20 common, genetically-encoded amino acids and that may be used to react efficiently and selectively to form stable covalent linkages.

The ability to incorporate non-genetically encoded amino acids into proteins permits the introduction of chemical functional groups that could provide valuable alternatives to the naturally-occurring functional groups, such as the epsilon —NH₂ of lysine, the sulfhydryl —SH of cysteine, the imino group of histidine, etc. Certain chemical functional groups such as carbonyl, alkyne, and azide moieties described herein are known to be inert to the functional groups found in the 20

common, genetically-encoded amino acids but react cleanly and efficiently to form stable linkages.

SUMMARY OF THE INVENTION

This invention provides human plasma protein (hPP) family members, including but not limited to, plasma proteins that function as carriers of other molecules. The hPP's that may be suitable for use in the present invention include but are not limited to those proteins listed in the following publications, which are incorporated by reference herein in their entirety: Anderson et al., *Molecular & Cellular Proteomics*, 3.4:311-326 (2004); and Ping et al., *Proteomics*, 5:3506-3519 (2005). Some of the known hPP's include but are not limited to, α 1-antichymotrypsin, antitrypsin, α 1-antitrypsin, pre-albumin, human albumin (human serum albumin), α 1-lipoprotein, A-gamma globulin, α 2-macroglobulin, α 1-microglobulin, α 2-microglobulin, β 2-microglobulin, Bence Jones protein, bile secretory component, complement protein 3, cholesteryl ester transfer protein, fatty acid binding protein, ferritin, ferritin H chain, fibrinogen, gastric inhibitory peptide, globulins, haptoglobulin, hemoglobin, hemoglobin A, hemoglobin A1C, hemoglobin F, glycated hemoglobin, pan hemoglobin, lactoferrin, lipase, lysozyme, mutY, myoglobin, cardiac myoglobin, orosmucoid, rheumatoid factor, secretin, serotonin, thyroglobulin, thyroxine, thyroxine binding globulin, triiodothyronine, transferring, vitamin D binding protein, and variant forms thereof, comprising one or more non-naturally encoded amino acids. This invention also provides human Fc (hFc) comprising one or more non-naturally encoded amino acids.

In some embodiments, the hPP or hFc comprises one or more post-translational modifications. In some embodiments, the hPP or hFc is linked to a linker, polymer, or biologically active molecule. In some embodiments, the hPP or hFc is linked to a bifunctional or multifunctional polymer, bifunctional or multifunctional linker, or at least one additional biologically active molecule.

In some embodiments, the non-naturally encoded amino acid is linked to a water soluble polymer. In some embodiments, the water soluble polymer comprises a poly(ethylene glycol) moiety. In some embodiments, the non-naturally encoded amino acid is linked to the water soluble polymer with a linker or is directly bonded to the water soluble polymer. In some embodiments, the poly(ethylene glycol) molecule is a bifunctional or multifunctional polymer. In some embodiments, the bifunctional or multifunctional polymer is linked to a second polypeptide. In some embodiments, the second polypeptide is a biologically active molecule.

In some embodiments, the hPP or hFc comprises at least two amino acids linked to a water soluble polymer, a linker, or a biologically active molecule. In some embodiments, at least one amino acid is a non-naturally encoded amino acid.

In some embodiments, the hPP comprising one or more non-naturally encoded amino acids is human albumin (hA), which is also known in the art as human serum albumin. The hA may be substituted with one or more non-naturally encoded amino acids at one or more of the 582 positions of the polypeptide sequence, including but not limited to one or more of the following positions: before position 1 (i.e. at the N-terminus), 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581, and after position 582 (i.e., at the carboxyl terminus of the protein) (SEQ ID NO: 1).

hFc may be substituted with one or more non-naturally encoded amino acids at one or more of the positions of the polypeptide sequence, including but not limited to, before position 1 (i.e. at the N-terminus) and at the N terminus (SEQ ID NO: 22).

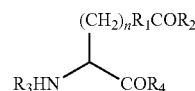
In some embodiments, the hPP or hFc comprises a substitution, addition or deletion that modulates affinity of the hPP or hFc for an hPP or hFc receptor or binding partner, including but not limited to, a protein, lipid, saccharide, polypeptide, small molecule, or nucleic acid. In some embodiments, the hPP or hFc comprises a substitution, addition, or deletion that increases the stability of the hPP or hFc when compared with the stability of the corresponding hPP or hFc without the substitution, addition, or deletion. In some embodiments, the hPP or hFc comprises a substitution, addition, or deletion that modulates the immunogenicity of the hPP or hFc when compared with the immunogenicity of the corresponding hPP or hFc without the substitution, addition, or deletion. In some embodiments, the hPP or hFc comprises a substitution, addition, or deletion that modulates serum half-life or circulation time of the hPP or hFc when compared with the serum half-life or circulation time of the corresponding hPP or hFc without the substitution, addition, or deletion.

In some embodiments, the hPP or hFc comprises a substitution, addition, or deletion that increases the aqueous solubility of the hPP or hFc when compared to aqueous solubility of the corresponding hPP or hFc without the substitution, addition, or deletion. In some embodiments, the hPP or hFc comprises a substitution, addition, or deletion that increases the expression of the hPP or hFc in a host cell or increases synthesis in vitro when compared to the expression or synthesis of the corresponding hPP or hFc without the substitution, addition, or deletion. The hPP or hFc comprising this substitution retains agonist activity and retains or improves expression levels in a host cell. In some embodiments, the hPP or hFc comprises a substitution, addition, or deletion that increases protease resistance of the hPP or hFc when compared to the protease resistance of the corresponding hPP or hFc without the substitution, addition, or deletion.

In some embodiments the amino acid substitutions in the hPP or hFc may be with naturally occurring or non-naturally occurring amino acids, provided that at least one substitution is with a non-naturally encoded amino acid.

In some embodiments, the non-naturally encoded amino acid comprises a carbonyl group, an acetyl group, an aminooxy group, a hydrazine group, a hydrazide group, a semicarbazide group, an azide group, an alkyne group, an aniline amino group, or a saccharide moiety.

In some embodiments, the non-naturally encoded amino acid comprises a carbonyl group. In some embodiments, the non-naturally encoded amino acid has the structure:

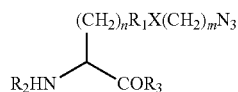


wherein n is 0-10; R₁ is an alkyl, aryl, substituted alkyl, or substituted aryl; R₂ is H, an alkyl, aryl, substituted alkyl, and substituted aryl; and R₃ is H, an amino acid, a polypeptide, or

an amino terminus modification group, and R_4 is H, an amino acid, a polypeptide, or a carboxy terminus modification group.

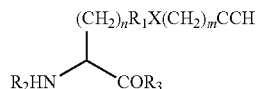
In some embodiments, the non-naturally encoded amino acid comprises an aminooxy group. In some embodiments, the non-naturally encoded amino acid comprises a hydrazide group. In some embodiments, the non-naturally encoded amino acid comprises a hydrazine group. In some embodiments, the non-naturally encoded amino acid residue comprises a semicarbazide group.

In some embodiments, the non-naturally encoded amino acid residue comprises an azide group. In some embodiments, the non-naturally encoded amino acid has the structure:



wherein n is 0-10; R_1 is an alkyl, aryl, substituted alkyl, substituted aryl or not present; X is O, N, S or not present; m is 0-10; R_2 is H, an amino acid, a polypeptide, or an amino terminus modification group, and R_3 is H, an amino acid, a polypeptide, or a carboxy terminus modification group.

In some embodiments, the non-naturally encoded amino acid comprises an alkyne group. In some embodiments, the non-naturally encoded amino acid has the structure:



wherein n is 0-10; R_1 is an alkyl, aryl, substituted alkyl, or substituted aryl; X is O, N, S or not present; m is 0-10, R_2 is H, an amino acid, a polypeptide, or an amino terminus modification group, and R_3 is H, an amino acid, a polypeptide, or a carboxy terminus modification group.

The present invention also provides isolated nucleic acids comprising a polynucleotide that hybridizes under stringent conditions to SEQ ID NO: 2, 20 or 23 wherein the polynucleotide comprises at least one selector codon. In some embodiments, the selector codon is selected from the group consisting of an amber codon, ochre codon, opal codon, a unique codon, a rare codon, a five-base codon, and a four-base codon.

The present invention also provides methods of making an hPP or hFc linked to a water soluble polymer. In some embodiments, the method comprises contacting an isolated hPP comprising a non-naturally encoded amino acid with a water soluble polymer comprising a moiety that reacts with the non-naturally encoded amino acid. In some embodiments, the non-naturally encoded amino acid incorporated into the hPP or hFc is reactive toward a water soluble polymer that is otherwise unreactive toward any of the 20 common amino acids. In some embodiments, the non-naturally encoded amino acid incorporated into the hPP or hFc is reactive toward a linker, polymer, or biologically active molecule that is otherwise unreactive toward any of the 20 common amino acids.

In some embodiments, the hPP or hFc linked to the water soluble polymer is made by reacting an hPP or hFc comprising a carbonyl-containing amino acid with a poly(ethylene glycol) molecule comprising an amino oxy, hydrazine, hydrazide or semicarbazide group. In some embodiments, the

aminooxy, hydrazine, hydrazide or semicarbazide group is linked to the poly(ethylene glycol) molecule through an amide linkage.

In some embodiments, the hPP or hFc linked to the water soluble polymer is made by reacting a poly(ethylene glycol) molecule comprising a carbonyl group with a polypeptide comprising a non-naturally encoded amino acid that comprises an aminooxy, hydrazine, hydrazide or semicarbazide group.

In some embodiments, the hPP or hFc linked to the water soluble polymer is made by reacting an hPP or hFc comprising an alkyne-containing amino acid with a poly(ethylene glycol) molecule comprising an azide moiety. In some embodiments, the azide or alkyne group is linked to the poly(ethylene glycol) molecule through an amide linkage.

In some embodiments, the hPP or hFc linked to the water soluble polymer is made by reacting an hPP or hFc comprising an azide-containing amino acid with a poly(ethylene glycol) molecule comprising an alkyne moiety. In some embodiments, the azide or alkyne group is linked to the poly(ethylene glycol) molecule through an amide linkage.

In some embodiments, the poly(ethylene glycol) molecule has a molecular weight of between about 0.1 kDa and about 100 kDa. In some embodiments, the poly(ethylene glycol) molecule has a molecular weight of between 0.1 kDa and 50 kDa.

In some embodiments, the poly(ethylene glycol) molecule is a branched polymer. In some embodiments, each branch of the poly(ethylene glycol) branched polymer has a molecular weight of between 1 kDa and 100 kDa, or between 1 kDa and 50 kDa.

In some embodiments, the water soluble polymer linked to the hPP comprises a polyalkylene glycol moiety. In some embodiments, the non-naturally encoded amino acid residue incorporated into the hPP or hFc comprises a carbonyl group, an aminooxy group, a hydrazide group, a hydrazine, a semicarbazide group, an azide group, or an alkyne group. In some embodiments, the non-naturally encoded amino acid residue incorporated into the hPP or hFc comprises a carbonyl moiety and the water soluble polymer comprises an aminooxy, hydrazide, hydrazine, or semicarbazide moiety. In some embodiments, the non-naturally encoded amino acid residue incorporated into the hPP or hFc comprises an alkyne moiety and the water soluble polymer comprises an azide moiety. In some embodiments, the non-naturally encoded amino acid residue incorporated into the hPP or hFc comprises an azide moiety and the water soluble polymer comprises an alkyne moiety.

The present invention also provides compositions comprising an hPP or hFc comprising a non-naturally encoded amino acid and a pharmaceutically acceptable carrier. In some embodiments, the non-naturally encoded amino acid is linked to a water soluble polymer.

The present invention also provides cells comprising a polynucleotide encoding the hPP or hFc comprising a selector codon. In some embodiments, the cells comprise an orthogonal RNA synthetase and/or an orthogonal tRNA for substituting a non-naturally encoded amino acid into the hPP or hFc.

The present invention also provides methods of making an hPP or hFc comprising a non-naturally encoded amino acid. In some embodiments, the methods comprise culturing cells comprising a polynucleotide or polynucleotides encoding an hPP or hFc, an orthogonal RNA synthetase and/or an orthogonal tRNA under conditions to permit expression of the hPP or hFc; and purifying the hPP or hFc from the cells and/or culture medium.

The present invention also provides methods of increasing therapeutic half-life, serum half-life or circulation time of hPP or hFc. The present invention also provides methods of modulating immunogenicity of hPP or hFc. In some embodiments, the methods comprise substituting a non-naturally encoded amino acid for any one or more amino acids in naturally occurring hPPs or hFc and/or linking the hPP or hFc to a linker, a polymer, a water soluble polymer, or a biologically active molecule.

The present invention also provides methods of treating a patient in need of such treatment with an effective amount of an hPP or hFc molecule of the present invention. In some embodiments, the methods comprise administering to the patient a therapeutically-effective amount of a pharmaceutical composition comprising an hPP or hFc comprising a non-naturally-encoded amino acid and a pharmaceutically acceptable carrier. In some embodiments, the non-naturally encoded amino acid is linked to a water soluble polymer.

The present invention also provides hPP comprising an amino acid sequence shown in SEQ ID NO: 1, or any other hPP polypeptide sequence, except that at least one amino acid is substituted by a non-naturally encoded amino acid. The present invention also provides hFc comprising an amino acid sequence shown in SEQ ID NO: 22, or any other hFc polypeptide sequence, except that at least one amino acid is substituted by a non-naturally encoded amino acid. In some embodiments, the non-naturally encoded amino acid is linked to a water soluble polymer. In some embodiments, the water soluble polymer comprises a poly(ethylene glycol) moiety. In some embodiments, the non-naturally encoded amino acid comprises a carbonyl group, an aminooxy group, a hydrazide group, a hydrazine group, a semicarbazide group, an azide group, or an alkyne group.

The present invention also provides pharmaceutical compositions comprising a pharmaceutically acceptable carrier and an hPP comprising the sequence shown in SEQ ID NO: 1, or any other hPP polypeptide sequence, wherein at least one amino acid is substituted by a non-naturally encoded amino acid. The present invention also provides pharmaceutical compositions comprising a pharmaceutically acceptable carrier and an hPP comprising the sequence shown in SEQ ID NO: 22 or any other hFc polypeptide sequence, wherein at least one amino acid is substituted by a non-naturally encoded amino acid. In some embodiments, the non-naturally encoded amino acid comprises a saccharide moiety. In some embodiments, the water soluble polymer is linked to the polypeptide via a saccharide moiety. In some embodiments, a linker, polymer, or biologically active molecule is linked to the hPP or hFc via a saccharide moiety.

The present invention also provides an hPP or hFc comprising a water soluble polymer linked by a covalent bond to the hPP or hFc at a single amino acid. In some embodiments, the water soluble polymer comprises a poly(ethylene glycol) moiety. In some embodiments, the amino acid covalently linked to the water soluble polymer is a non-naturally encoded amino acid present in the polypeptide.

The present invention provides an hPP or hFc comprising at least one linker, polymer, or biologically active molecule, wherein said linker, polymer, or biologically active molecule is attached to the polypeptide through a functional group of a non-naturally encoded amino acid ribosomally incorporated into the polypeptide. In some embodiments, the polypeptide is monoPEGylated. The present invention also provides an hPP or hFc comprising a linker, polymer, or biologically active molecule that is attached to one or more non-naturally

encoded amino acid wherein said non-naturally encoded amino acid is ribosomally incorporated into the polypeptide at pre-selected sites.

In another embodiment, conjugation of the hPP or hFc comprising one or more non-naturally occurring amino acids to another molecule, including but not limited to PEG, provides substantially purified hPP or hFc due to the unique chemical reaction utilized for conjugation to the non-natural amino acid. In another embodiment, one or more non-naturally encoded amino acids are incorporated into the amino acid sequence of an hPP or hFc provides advantages for purification of the hPP or hFc utilizing the functional group of the non-naturally encoded amino acid. Conjugation of hPP or hFc comprising one or more non-naturally encoded amino acids to another molecule, such as PEG, may be performed with other purification techniques performed prior to or following the conjugation step to provide substantially pure hPP or hFc. In another embodiment substitution of a non-naturally encoded amino acid into the amino acid sequence of an hPP or hFc modulates the pKa of the polypeptide, which in turn modulates the conjugation reaction conditions, rate or efficiency when conjugating the hPP or hFc to other molecules. In some embodiments the hPP or hFc comprising the non-naturally encoded amino acid exhibits modulated binding characteristics, such as increased or decreased binding strength, when contacted with a binding partner. In some embodiments the hPP or hFc comprising the non-naturally encoded amino acid exhibits modulated tissue binding or tissue distribution characteristics when compared to the same hPP or hFc lacking the non-naturally encoded amino acid. In some embodiments the hPP or hFc comprising the non-naturally encoded amino acid has modulated stability properties when the hPP or hFc is formulated for pharmaceutical uses.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1—The average Cx values for hA amino acids is shown.

FIG. 2—A model of hA and certain amino acids positions are shown.

FIG. 3—A table of selected amino acid positions in hA for substitution with non-naturally encoded amino acids is shown.

FIG. 4—The expression of recombinant human albumin in yeast host cells is shown by coomassie stained polyacrylamide gel electrophoresis.

FIG. 5—The expression of hA containing a non-naturally encoded amino acid in the polypeptide sequence is shown by coomassie stained polyacrylamide gel electrophoresis.

FIG. 6, Panel A—Reduced samples of purified Fc (WT) and D1pAF-substituted Fc (D1pAF) incubated in the presence (+) or absence (−) of 5K amino-oxy poly(ethylene)-glycol (PEG) were analyzed by SDS-PAGE.

FIG. 6, Panel B—Non-reduced samples of purified Fc (WT) and D1pAF-substituted Fc (D1pAF) incubated in the presence (+) or absence (−) of 5K amino-oxy poly(ethylene)-glycol (PEG) were analyzed by SDS-PAGE.

FIG. 7A—The polynucleotide sequence of a wild type Fc is shown.

FIG. 7B—The polypeptide sequence of a wild type Fc is shown.

FIG. 7C—The polypeptide sequence of a mature Fc is shown.

FIG. 7D—The polynucleotide sequence encoding a mature Fc is shown.

FIG. 8A—The incorporation of non-natural amino acid into hA is shown in a coomassie stained polyacrylamide gel.

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FIG. 8B—The incorporation of non-natural amino acids into hA is shown in a Western blot.

FIG. 8C—The incorporation of non-natural amino acids into hA is shown in a Western blot.

FIG. 9—The production of PEGylated hA is shown by Western blot.

FIG. 10 Panel A and FIG. 10 Panel B—Peptide mapping results for hA comprising a non-natural amino acid, and wild type hA, respectively, are shown.

FIG. 11A—Mass spectroscopy results of hA comprising non-natural amino acid (pAF, or para acetyl phenylalanine) is shown.

FIG. 11B—The predicted ion masses for the amino acids of hA, including non-natural amino acid pAF (para acetyl phenylalanine) is shown.

DEFINITIONS

It is to be understood that this invention is not limited to the particular methodology, protocols, cell lines, constructs, and reagents described herein and as such may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which will be limited only by the appended claims.

As used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural reference unless the context clearly indicates otherwise. Thus, for example, reference to an “hPP” or “hA” or “hFc” is a reference to one or more such proteins and includes equivalents thereof known to those of ordinary skill in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices, and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described.

All publications and patents mentioned herein are incorporated herein by reference for the purpose of describing and disclosing, for example, the constructs and methodologies that are described in the publications, which might be used in connection with the presently described invention. The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention or for any other reason.

The term “substantially purified” refers to an “hPP” or “hA” or hFc polypeptide that may be substantially or essentially free of components that normally accompany or interact with the protein as found in its naturally occurring environment, i.e. a native cell, or host cell in the case of recombinantly produced an “hPP” or “hA” or “hFc” polypeptide. An “hPP” or “hA” or “hFc” polypeptide that may be substantially free of cellular material includes preparations of protein having less than about 30%, less than about 25%, less than about 20%, less than about 15%, less than about 10%, less than about 5%, less than about 4%, less than about 3%, less than about 2%, or less than about 1% (by dry weight) of contaminating protein. When an “hPP” or “hA” or “hFc” polypeptide or variant thereof is recombinantly produced by the host cells, the protein may be present at about 30%, about 25%, about 20%, about 15%, about 10%, about 5%, about 4%, about 3%, about 2%, or about 1% or less of the dry weight of the cells. When an “hPP” or “hA” or “hFc” polypeptide or variant thereof is recombinantly produced by the host cells, the pro-

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tein may be present in the culture medium at about 5 g/L, about 4 g/L, about 3 g/L, about 2 g/L, about 1 g/L, about 750 mg/L, about 500 mg/L, about 250 mg/L, about 100 mg/L, about 50 mg/L, about 10 mg/L, or about 1 mg/L or less of the dry weight of the cells. Thus, “substantially purified” “hPP” or “hA” or “hFc” polypeptide as produced by the methods of the present invention may have a purity level of at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, specifically, a purity level of at least about 75%, 80%, 85%, and more specifically, a purity level of at least about 90%, a purity level of at least about 95%, a purity level of at least about 99% or greater as determined by appropriate methods such as SDS/PAGE analysis, RP-HPLC, SEC, and capillary electrophoresis.

A “recombinant host cell” or “host cell” refers to a cell that includes an exogenous polynucleotide, regardless of the method used for insertion, for example, direct uptake, transduction, f-mating, or other methods known in the art to create recombinant host cells. The exogenous polynucleotide may be maintained as a nonintegrated vector, for example, a plasmid, or alternatively, may be integrated into the host genome.

As used herein, the term “medium” or “media” includes any culture medium, solution, solid, semi-solid, or rigid support that may support or contain any host cell, including bacterial host cells, yeast host cells, insect host cells, plant host cells, eukaryotic host cells, mammalian host cells, CHO cells, prokaryotic host cells, *E. coli*, or *Pseudomonas* host cells, and cell contents. Thus, the term may encompass medium in which the host cell has been grown, e.g., medium into which an “hPP” or “hA” or “hFc” polypeptide has been secreted, including medium either before or after a proliferation step. The term also may encompass buffers or reagents that contain host cell lysates, such as in the case where an “hPP” or “hA” or “hFc” polypeptide is produced intracellularly and the host cells are lysed or disrupted to release the “hPP” or “hA” or “hFc” polypeptide.

“Reducing agent,” as used herein with respect to protein refolding, is defined as any compound or material which maintains sulphydryl groups in the reduced state and reduces intra- or intermolecular disulfide bonds. Suitable reducing agents include, but are not limited to, dithiothreitol (DTT), 2-mercaptoethanol, dithioerythritol, cysteine, cysteamine (2-aminoethanethiol), and reduced glutathione. It is readily apparent to those of ordinary skill in the art that a wide variety of reducing agents are suitable for use in the methods and compositions of the present invention.

“Oxidizing agent,” as used herein with respect to protein refolding, is defined as any compound or material which is capable of removing an electron from a compound being oxidized. Suitable oxidizing agents include, but are not limited to, oxidized glutathione, cystine, cystamine, oxidized dithiothreitol, oxidized erythreitol, and oxygen. It is readily apparent to those of ordinary skill in the art that a wide variety of oxidizing agents are suitable for use in the methods of the present invention.

“Denaturing agent” or “denaturant,” as used herein, is defined as any compound or material which will cause a reversible unfolding of a protein. The strength of a denaturing agent or denaturant will be determined both by the properties and the concentration of the particular denaturing agent or denaturant. Suitable denaturing agents or denaturants may be chaotropes, detergents, organic solvents, water miscible solvents, phospholipids, or a combination of two or more such agents. Suitable chaotropes include, but are not limited to, urea, guanidine, and sodium thiocyanate. Useful detergents

may include, but are not limited to, strong detergents such as sodium dodecyl sulfate, or polyoxyethylene ethers (e.g. Tween or Triton detergents), Sarkosyl, mild non-ionic detergents (e.g., digitonin), mild cationic detergents such as N->2, 3-(Dioleyoxy)-propyl-N,N,N-trimethylammonium, mild ionic detergents (e.g. sodium cholate or sodium deoxycholate) or zwitterionic detergents including, but not limited to, sulfobetaines (Zwittergent), 3-(3-chloramidopropyl)dimethylammonio-1-propane sulfate (CHAPS), and 3-(3-chloramidopropyl)dimethylammonio-2-hydroxy-1-propane sulfonate (CHAPSO). Organic, water miscible solvents such as acetonitrile, lower alkanols (especially C₂-C₄ alkanols such as ethanol or isopropanol), or lower alkandiol (especially C₂-C₄ alkandiol such as ethylene-glycol) may be used as denaturants. Phospholipids useful in the present invention may be naturally occurring phospholipids such as phosphatidylethanolamine, phosphatidylcholine, phosphatidylserine, and phosphatidylinositol or synthetic phospholipid derivatives or variants such as dihexanoylphosphatidylcholine or diheptanoylphosphatidylcholine.

"Refolding," as used herein describes any process, reaction or method which transforms disulfide bond containing polypeptides from an improperly folded or unfolded state to a native or properly folded conformation with respect to disulfide bonds.

"Cofolding," as used herein, refers specifically to refolding processes, reactions, or methods which employ at least two polypeptides which interact with each other and result in the transformation of unfolded or improperly folded polypeptides to native, properly folded polypeptides.

As used herein, "human plasma protein or polypeptide" or "hPP" includes those polypeptides and proteins that are found in normal human blood plasma, including hPP analogs, hPP isoforms, hPP mimetics, hPP fragments, hybrid hPP proteins, fusion proteins, oligomers and multimers, homologues, glycosylation pattern variants, variants, splice variants, and muteins, thereof, regardless of the biological activity of same, and further regardless of the method of synthesis or manufacture thereof including, but not limited to, recombinant (whether produced from cDNA, genomic DNA, synthetic DNA or other form of nucleic acid), in vitro, in vivo, by microinjection of nucleic acid molecules, synthetic, transgenic, and gene activated methods. A variety of hPP's are known in the art and can be found in Anderson et al., *Molecular & Cellular Proteomics*, 3:4311-326 (2004); and Ping et al., *Proteomics*, 5:3506-3519 (2005), which are incorporated by reference herein. The hPP useful in the present invention may include but are not limited to α 1-antichymotrypsin, antitrypsin, α 1-antitrypsin, pre-albumin, human albumin (human serum albumin), α 1-lipoprotein, A-gamma globulin, α 2-macroglobulin, α 1-microglobulin, α 2-microglobulin, β 2-microglobulin, Bence Jones protein, bile secretory component, complement protein 3, cholesteryl ester transfer protein, fatty acid binding protein, ferritin, ferritin H chain, fibrinogen, gastric inhibitory peptide, globulins, haptoglobulin, hemoglobin, hemoglobin A, hemoglobin A1C, hemoglobin F, glycated hemoglobin, pan hemoglobin, lactoferrin, lipase, lysozyme, mutY, myoglobin, cardiac myoglobin, orosmucoid, rheumatoid factor, secretin, serotonin, thyroglobulin, thyroxine, thyroxine binding globulin, triiodothyronine, transferring, vitamin D binding protein, and variant forms thereof.

As used herein, "albumin" refers collectively to albumin protein or amino acid sequence, or an albumin fragment or variant, having one or more functional activities (e.g., biological activities) of albumin. In particular, "albumin" refers to human albumin ("hA") or fragments thereof especially the

mature form of human albumin as shown in SEQ ID NO:1, or albumin from other vertebrates such as bovine, porcine, equine, canine, feline, or avian, or fragments thereof, or analogs or variants of these molecules or fragments thereof. The amino acid sequence and the nucleotide sequence of hA are known in the art and disclosed, for example, in U.S. Pat. Nos. 5,879,907; 5,756,313; 5,707,828; 5,986,062; 5,521,287; 5,612,197; 5,440,18; 5,759,819; and 5,648,243, which are incorporated by reference herein.

In some embodiments, the human serum albumin protein used in the present invention contains one or both of the following sets of point mutations with reference to SEQ ID NO:1: Leu-407 to Ala, Leu-408 to Val, Val-409 to Ala, and Arg-410 to Ala; or Arg-410 to Ala, Lys-413 to Gln, and Lys-414 to Gln (see, e.g., International Patent Publication No. WO95/23857, hereby incorporated by reference herein in its entirety). In other embodiments, albumin fusion proteins of the present invention that contain one or both of above-described sets of point mutations have improved stability/resistance to yeast Yap3p proteolytic cleavage, allowing increased production of recombinant albumin fusion proteins expressed in yeast host cells.

As used herein, a portion of hA sufficient to prolong the therapeutic activity, circulation time, or shelf-life of a therapeutic product refers to a portion of hA sufficient in length or structure to stabilize or prolong the therapeutic activity of the protein. The albumin portion of the proteins may comprise the full length of the hA sequence as described herein, or may include one or more fragments thereof that are capable of providing the desired activity. Such hA fragments may be of 10 or more amino acids in length or may include about 15, 20, 25, 30, 50, 100 or more contiguous amino acids from the hA sequence or may include part or all of specific domains of hA. For example, one or more fragments of hA spanning the first two immunoglobulin-like domains may be used. Examples of truncated forms of hA may be found in U.S. Pat. No. 5,380,712, which is incorporated by reference herein.

The albumin portion of the albumin fusion proteins of the invention may be a variant of normal hA. The therapeutic protein portion of the albumin fusion proteins of the invention may also be variants of the therapeutic proteins as described herein. The term "variants" includes insertions, deletions and substitutions, either conservative or non conservative, where such changes do not substantially alter one or more of the oncotic, useful ligand-binding and non-immunogenic properties of albumin, or the active site, or active domain which confers the therapeutic activities of the therapeutic proteins.

In particular, the hA proteins of the invention may include naturally occurring polymorphic variants of hA and fragments of hA, for example those fragments disclosed in EP 322 094. The albumin may be derived from any vertebrate, especially any mammal, for example human, cow, sheep, or pig. Non-mammalian albumins include, but are not limited to, hen and salmon. The albumin portion of the albumin fusion protein may be from a different animal than a molecule that may be coupled to the hA. An hA fragment or variant may also be utilized in the present invention. The hA variant may consist of or alternatively comprise at least one complete structural domain of hA, for example domains 1 (amino acids 1-194 of SEQ ID NO:1), 2 (amino acids 195-387 of SEQ ID NO:1), 3 (amino acids 388-585 of SEQ ID NO:1), 1/2 (1-387 of SEQ ID NO:1), 2/3 (195-585 of SEQ ID NO:1) or 1/3 (amino acids 1-194 of SEQ ID NO:1 and amino acids 388-585 of SEQ ID NO:1). Each domain is itself made up of two homologous subdomains namely 1-105, 120-194, 195-291, 316-387, 388-491 and 512-585, with flexible inter-subdomain linker regions comprising residues Lys 106 to Glu 119,

Glu292 to Val315 and Glu492 to Ala511. Preferably, the hA portion of an hA protein of the present invention comprises at least one subdomain or domain of hA or conservative modifications thereof. If the hA is based on subdomains, some or all of the adjacent linker is preferably used to link to another molecule such as a linker, polymer, or biologically active molecule.

For the complete full-length naturally-occurring hA amino acid sequence, see SEQ ID NO: 1 herein. In some embodiments, hA polypeptides of the invention are substantially identical to SEQ ID NO: 1. For the complete nucleic acid sequence encoding hA, see SEQ ID NO: 2 herein. In some embodiments, hA polypeptides of the invention are encoded by a nucleic acid sequence substantially identical to SEQ ID NO: 2.

The term "hA" also includes the pharmaceutically acceptable salts and prodrugs, and prodrugs of the salts, polymorphs, hydrates, solvates, biologically-active fragments, biologically active variants and stereoisomers of the naturally-occurring hA as well as agonist, mimetic, and antagonist variants of the naturally-occurring hA and polypeptide fusions thereof. Fusions comprising additional amino acids at the amino terminus, carboxyl terminus, or both, are encompassed by the term "hA polypeptide."

Antibodies are proteins, which exhibit binding specificity to a specific antigen. Native antibodies are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain at one end (V_L) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light and heavy chain variable domains.

The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are responsible for the binding specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed through the variable domains of antibodies. It is concentrated in three segments called Complementarity Determining Regions (CDRs) both in the light chain and the heavy chain variable domains. The more highly conserved portions of the variable domains are called the framework regions (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a β -sheet configuration, connected by three or four CDRs, which form loops connecting, and in some cases forming part of, the β -sheet structure. The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)).

The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions. Depending on the amino acid sequence of the constant region of their heavy chains, antibodies or immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, and

several of these may be further divided into subclasses (isotypes), e.g. IgG1, IgG2, IgG3, and IgG4; IgA1 and IgA2. The heavy chain constant regions that correspond to the different classes of immunoglobulins are called α , δ , ϵ , γ and μ , respectively. Of the various human immunoglobulin classes, only human IgG1, IgG2, IgG3 and IgM are known to activate complement.

In vivo, affinity maturation of antibodies is driven by antigen selection of higher affinity antibody variants which are made primarily by somatic hypermutagenesis. A "repertoire shift" also often occurs in which the predominant germline genes of the secondary or tertiary response are seen to differ from those of the primary or secondary response.

The affinity maturation process of the immune system may be replicated by introducing mutations into antibody genes in vitro and using affinity selection to isolate mutants with improved affinity. Such mutant antibodies can be displayed on the surface of filamentous bacteriophage or microorganisms such as yeast, and antibodies can be selected by their affinity for antigen or by their kinetics of dissociation (off-rate) from antigen. Hawkins et al. J. Mol. Biol. 226:889-896 (1992). CDR walking mutagenesis has been employed to affinity mature human antibodies which bind the human envelope glycoprotein gp120 of human immunodeficiency virus type 1 (HIV-1) (Barbas I Ig I et al. PNAS (USA) 91: 3809-3813 (1994); and Yang et al. J. Mol. Biol. 254:392-403 (1995)); and an anti-c-erbB-2 single chain Fv fragment (Schier et al. J. Mol. Biol. 263:551567 (1996)). Antibody chain shuffling and CDR mutagenesis were used to affinity mature a high-affinity human antibody directed against the third hypervariable loop of HIV (Thompson et al. J. Mol. Biol. 256:77-88 (1996)). Balint and Larrick Gene 137:109-118 (1993) describe a computer-assisted oligodeoxyribonucleotide-directed scanning mutagenesis whereby all CDRs of a variable region gene are simultaneously and thoroughly searched for improved variants. An $\alpha\beta$ 3-specific humanized antibody was affinity matured using an initial limited mutagenesis strategy in which every position of all six CDRs was mutated followed by the expression and screening of a combinatorial library including the highest affinity mutants (Wu et al. PNAS (USA) 95: 6037-6-42 (1998)). Phage displayed antibodies are reviewed in Chiswell and McCafferty TIBTECH 10:80-84 (1992); and Rader and Barbas III Current Opinion in Biotech. 8:503-508 (1997). In each case where mutant antibodies with improved affinity compared to a parent antibody are reported in the above references, the mutant antibody has amino acid substitutions in a CDR.

By "affinity maturation" herein is meant the process of enhancing the affinity of an antibody for its antigen. Methods for affinity maturation include but are not limited to computational screening methods and experimental methods.

By "antibody" herein is meant a protein consisting of one or more polypeptides substantially encoded by all or part of the antibody genes. The immunoglobulin genes include, but are not limited to, the kappa, lambda, alpha, gamma (IgG1, IgG2, IgG3, and IgG4), delta, epsilon and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Antibody herein is meant to include full-length antibodies and antibody fragments, and include antibodies that exist naturally in any organism or are engineered (e.g. are variants).

By "antibody fragment" is meant any form of an antibody other than the full-length form. Antibody fragments herein include antibodies that are smaller components that exist within full-length antibodies, and antibodies that have been engineered. Antibody fragments include but are not limited to Fv, Fc, Fab, and (Fab')₂, single chain Fv (scFv), diabodies,

triabodies, tetrabodies, bifunctional hybrid antibodies, CDR1, CDR2, CDR3, combinations of CDR's, variable regions, framework regions, constant regions, and the like (Maynard & Georgiou, 2000, *Annu. Rev. Biomed. Eng.* 2:339-76; Hudson, 1998, *Curr. Opin. Biotechnol.* 9:3 95-402).

By "Fc" herein is meant the portions of an antibody that are comprised of immunoglobulin domains C γ 2 and C γ 3 (C γ 2 and C γ 3). Fc may also include any residues which exist in the N-terminal hinge between C γ 2 and C γ 1 (C γ 1). Fc may refer to this region in isolation, or this region in the context of an antibody or antibody fragment. Fc also includes any modified forms of Fc, including but not limited to the native monomer, the native dimer (disulfide bond linked), modified dimers (disulfide and/or non-covalently linked), and modified monomers (i.e., derivatives). "hFc" refers to human Fc.

By "full-length antibody" herein is meant the structure that constitutes the natural biological form of an antibody H and/or L chain. In most mammals, including humans and mice, this form is a tetramer and consists of two identical pairs of two immunoglobulin chains, each pair having one light and one heavy chain, each light chain comprising immunoglobulin domains V_L and C_L, and each heavy chain comprising immunoglobulin domains V_H, C γ 1, C γ 2, and C γ 3. In each pair, the light and heavy chain variable regions (V_L and V_H) are together responsible for binding to an antigen, and the constant regions (C_L, C γ 1, C γ 2, and C γ 3, particularly C γ 2, and C γ 3) are responsible for antibody effector functions. In some mammals, for example in camels and llamas, full-length antibodies may consist of only two heavy chains, each heavy chain comprising immunoglobulin domains V_H, C γ 2, and C γ 3.

By "immunoglobulin (Ig)" herein is meant a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. Immunoglobulins include but are not limited to antibodies. Immuno globulins may have a number of structural forms, including but not limited to full-length antibodies, antibody fragments, and individual immunoglobulin domains including but not limited to V_H, C γ 1, C γ 2, C γ 3, V_L, and C_L.

By "immunoglobulin (Ig) domain" herein is meant a protein domain consisting of a polypeptide substantially encoded by an immunoglobulin gene. Ig domains include but are not limited to V_H, C γ 1, C γ 2, C γ 3, V_L, and C_L.

By "variant protein sequence" as used herein is meant a protein sequence that has one or more residues that differ in amino acid identity from another similar protein sequence. Said similar protein sequence may be the natural wild type protein sequence, or another variant of the wild type sequence. In general, a starting sequence is referred to as a "parent" sequence, and may either be a wild type or variant sequence. For example, preferred embodiments of the present invention may utilize humanized parent sequences upon which computational analyses are done to make variants.

By "variable region" of an antibody herein is meant a polypeptide or polypeptides composed of the V_H immunoglobulin domain, the V_L immunoglobulin domains, or the V_H and V_L immunoglobulin domains (including variants). Variable region may refer to this or these polypeptides in isolation, as an Fv fragment, as a scFv fragment, as this region in the context of a larger antibody fragment, or as this region in the context of a full-length antibody or an alternative, non-antibody scaffold molecule.

The present invention may be applied to antibodies obtained from a wide range of sources. The antibody may be substantially encoded by an antibody gene or antibody genes from any organism, including but not limited to humans,

mice, rats, rabbits, camels, llamas, dromedaries, monkeys, particularly mammals and particularly human and particularly mice and rats. In one embodiment, the antibody may be fully human, obtained for example from a patient or subject, by using transgenic mice or other animals (Bruggemann & Taussig, 1997, *Curr. Opin. Biotechnol.* 8:455-458) or human antibody libraries coupled with selection methods (Griffiths & Duncan, 1998, *Curr. Opin. Biotechnol.* 9:102-108). The antibody may be from any source, including artificial or naturally occurring. For example the present invention may utilize an engineered antibody, including but not limited to chimeric antibodies and humanized antibodies (Clark, 2000, *Immunol. Today* 21:397-402) or derived from a combinatorial library. In addition, the antibody being optimized may be an engineered variant of an antibody that is substantially encoded by one or more natural antibody genes. For example, in one embodiment the antibody being optimized is an antibody that has been identified by affinity maturation.

As used herein, "hFc" or "human Fc" or "hFc polypeptides" includes hFc analogs, hFc isoforms, hFc mimetics, hFc fragments, hybrid hFc proteins, fusion proteins, oligomers and multimers, homologues, glycosylation pattern variants, variants, splice variants, and muteins, thereof, regardless of the biological activity of same, and further regardless of the method of synthesis or manufacture thereof including, but not limited to, recombinant (whether produced from cDNA, genomic DNA, synthetic DNA or other form of nucleic acid), in vitro, in vivo, by microinjection of nucleic acid molecules, synthetic, transgenic, and gene activated methods. A variety of hFc's are known in the art.

The term "hFc" also includes the pharmaceutically acceptable salts and prodrugs, and prodrugs of the salts, polymorphs, hydrates, solvates, biologically-active fragments, biologically active variants and stereoisomers of hFc as well as agonist, mimetic, and antagonist variants of the hFc and polypeptide fusions thereof. Fusions comprising additional amino acids at the amino terminus, carboxyl terminus, or both, are encompassed by the term "hFc polypeptide."

Various references disclose modification of polypeptides by polymer conjugation or glycosylation. The term "hPP polypeptide" or "hA polypeptide" or "hFc polypeptide" includes polypeptides conjugated to a polymer such as PEG and may be comprised of one or more additional derivitizations of cysteine, lysine, or other residues. In addition, the hPP polypeptide or hA or hFc polypeptide may comprise a linker or polymer, wherein the amino acid to which the linker or polymer is conjugated may be a non-natural amino acid according to the present invention, or may be conjugated to a naturally encoded amino acid utilizing techniques known in the art such as coupling to lysine or cysteine.

The term "hPP polypeptide" or "hA polypeptide" or "hFc polypeptide" also includes glycosylated forms, such as but not limited to, polypeptides glycosylated at any amino acid position, N-linked or O-linked glycosylated forms of the polypeptide. Variants containing single nucleotide changes are also considered as biologically active variants of hPP polypeptide or hA polypeptide or hFc polypeptide. In addition, splice variants are also included. The term hPP polypeptide or hA polypeptide or hFc polypeptide also includes hPP or hA or hFc polypeptide heterodimers, homodimers, heteromultimers, or homomultimers of any one or more hPP or hA or hFc polypeptides or any other polypeptide, protein, carbohydrate, polymer, small molecule, linker, ligand, or other biologically active molecule of any type, linked by chemical means or expressed as a fusion protein, as well as polypeptide analogues containing, for example, specific deletions or other modifications yet maintain biological activity.

All references to amino acid positions in hA described herein are based on the position in SEQ ID NO: 1, unless otherwise specified. Those of skill in the art will appreciate that amino acid positions corresponding to positions in SEQ ID NO: 1 or any other hA sequence can be readily identified in any other hA molecule such as hA fusions, variants, fragments, etc. For example, sequence alignment programs such as BLAST can be used to align and identify a particular position in a protein that corresponds with a position in SEQ ID NO: 1, 2, or other hA sequence. Substitutions, deletions or additions of amino acids described herein in reference to SEQ ID NO: 1, or other hA sequence are intended to also refer to substitutions, deletions or additions in corresponding positions in hA fusions, variants, fragments, etc. described herein or known in the art and are expressly encompassed by the present invention.

All references to amino acid positions in hFc described herein are based on the position in SEQ ID NO: 22, unless otherwise specified. Those of skill in the art will appreciate that amino acid positions corresponding to positions in SEQ ID NO: 22 or any other hFc sequence can be readily identified in any other hFc molecule such as hFc fusions, variants, fragments, etc. For example, sequence alignment programs such as BLAST can be used to align and identify a particular position in a protein that corresponds with a position in SEQ ID NO: 20, 21, 22, 23, or other hFc sequence. Substitutions, deletions or additions of amino acids described herein in reference to SEQ ID NO: 22, or other hFc sequence are intended to also refer to substitutions, deletions or additions in corresponding positions in hFc fusions, variants, fragments, etc. described herein or known in the art and are expressly encompassed by the present invention.

A “non-naturally encoded amino acid” refers to an amino acid that is not one of the 20 common amino acids or pyrrolysine or selenocysteine. Other terms that may be used synonymously with the term “non-naturally encoded amino acid” are “non-natural amino acid,” “unnatural amino acid,” “non-naturally-occurring amino acid,” and variously hyphenated and non-hyphenated versions thereof. The term “non-naturally encoded amino acid” also includes, but is not limited to, amino acids that occur by modification (e.g. post-translational modifications) of a naturally encoded amino acid (including but not limited to, the 20 common amino acids or pyrrolysine and selenocysteine) but are not themselves naturally incorporated into a growing polypeptide chain by the translation complex. Examples of such non-naturally-occurring amino acids include, but are not limited to, N-acetylglucosaminyl-L-serine, N-acetylglucosaminyl-L-threonine, and O-phosphotyrosine.

An “amino terminus modification group” refers to any molecule that can be attached to the amino terminus of a polypeptide. Similarly, a “carboxy terminus modification group” refers to any molecule that can be attached to the carboxy terminus of a polypeptide. Terminus modification groups include, but are not limited to, various water soluble polymers, peptides or proteins such as serum albumin, or other moieties that increase serum half-life of peptides.

The terms “functional group”, “active moiety”, “activating group”, “leaving group”, “reactive site”, “chemically reactive group” and “chemically reactive moiety” are used in the art and herein to refer to distinct, definable portions or units of a molecule. The terms are somewhat synonymous in the chemical arts and are used herein to indicate the portions of molecules that perform some function or activity and are reactive with other molecules.

The term “linkage” or “linker” is used herein to refer to groups or bonds that normally are formed as the result of a

chemical reaction and typically are covalent linkages. Hydrolytically stable linkages means that the linkages are substantially stable in water and do not react with water at useful pH values, including but not limited to, under physiological conditions for an extended period of time, perhaps even indefinitely. Hydrolytically unstable or degradable linkages mean that the linkages are degradable in water or in aqueous solutions, including for example, blood. Enzymatically unstable or degradable linkages mean that the linkage can be degraded by one or more enzymes. As understood in the art, PEG and related polymers may include degradable linkages in the polymer backbone or in the linker group between the polymer backbone and one or more of the terminal functional groups of the polymer molecule. For example, ester linkages formed by the reaction of PEG carboxylic acids or activated PEG carboxylic acids with alcohol groups on a biologically active agent generally hydrolyze under physiological conditions to release the agent. Other hydrolytically degradable linkages include, but are not limited to, carbonate linkages; imine linkages resulted from reaction of an amine and an aldehyde; phosphate ester linkages formed by reacting an alcohol with a phosphate group; hydrazone linkages which are reaction product of a hydrazide and an aldehyde; acetal linkages that are the reaction product of an aldehyde and an alcohol; orthoester linkages that are the reaction product of a formate and an alcohol; peptide linkages formed by an amine group, including but not limited to, at an end of a polymer such as PEG, and a carboxyl group of a peptide; and oligonucleotide linkages formed by a phosphoramidite group, including but not limited to, at the end of a polymer, and a 5' hydroxyl group of an oligonucleotide.

The term “biologically active molecule”, “biologically active moiety” or “biologically active agent” when used herein means any substance which can affect any physical or biochemical properties of a biological system, pathway, molecule, or interaction relating to an organism, including but not limited to, viruses, bacteria, bacteriophage, transposon, prion, insects, fungi, plants, animals, and humans. In particular, as used herein, biologically active molecules include, but are not limited to, any substance intended for diagnosis, cure, mitigation, treatment, or prevention of disease in humans or other animals, or to otherwise enhance physical or mental well-being of humans or animals. Examples of biologically active molecules include, but are not limited to, peptides, proteins, enzymes, small molecule drugs, hard drugs, soft drugs, carbohydrates, inorganic atoms or molecules, dyes, lipids, nucleosides, radionuclides, oligonucleotides, toxins, cells, viruses, liposomes, microparticles and micelles. Classes of biologically active agents that are suitable for use with the invention include, but are not limited to, drugs, prodrugs, radionuclides, imaging agents, polymers, antibiotics, fungicides, anti-viral agents, anti-inflammatory agents, anti-tumor agents, cardiovascular agents, anti-anxiety agents, hormones, growth factors, steroidal agents, microbially derived toxins, and the like. Biologically active molecules encompasses a variety of polypeptides including, but not limited to, Representative non-limiting classes of polypeptides useful in the present invention include those falling into the following therapeutic categories: adrenocorticotrophic hormone peptides, adrenomedullin peptides, allatostatin peptides, amylin peptides, amyloid beta-protein fragment peptides, angiotensin peptides, antibiotic peptides, antigenic polypeptides, anti-microbial peptides, apoptosis related peptides, atrial natriuretic peptides, bag cell peptides, bombesin peptides, bone GLA peptides, bradykinin peptides, brain natriuretic peptides, C-peptides, C-type natriuretic peptides, calcitonin peptides, calcitonin gene related peptides, CART

peptides, casomorphin peptides, chemotactic peptides, cholecystokinin peptides, colony-stimulating factor peptides, corticotropin releasing factor peptides, cortistatin peptides, cytokine peptides, dermorphin peptides, dynorphin peptides, endorphin peptides, endothelin peptides, ETa receptor antagonist peptides, ETb receptor antagonist peptides, enkephalin peptides, fibronectin peptides, galanin peptides, gastrin peptides, glucagon peptides, Gn-RH associated peptides, growth factor peptides, growth hormone peptides, GTP-binding protein fragment peptides, guanylin peptides, inhibin peptides, insulin peptides, interleukin peptides, laminin peptides, leptin peptides, leucokinin peptides, luteinizing hormone-releasing hormone peptides, mastoparan peptides, mast cell degranulating peptides, melanocyte stimulating hormone peptides, morphiceptin peptides, motilin peptides, neuro-peptides, neuropeptide Y peptides, neurotropic factor peptides, orexia peptides, opioid peptides, oxytocin peptides, PACAP peptides, pancreastatin peptides, pancreatic polypeptides, parathyroid hormone peptides, parathyroid hormone-related peptides, peptide T peptides, prolactin-releasing peptides, peptide YY peptides, renin substrate peptides, secretin peptides, somatostatin peptides, substance P peptides, tachykinin peptides, thyrotropin-releasing hormone peptides, toxin peptides, vasoactive intestinal peptides, vasopressin peptides, and virus related peptides. (see U.S. Pat. No. 6,858,580).

Examples of biologically active molecules that are polypeptides include, but are not limited to, pituitary hormones such as vasopressin, oxytocin, melanocyte stimulating hormones, adrenocorticotrophic hormones, growth hormones; hypothalamic hormones such as growth hormone releasing factor, corticotropin releasing factor, prolactin releasing peptides, gonadotropin releasing hormone and its associated peptides, luteinizing hormone release hormones, thyrotropin releasing hormone, orexins, and somatostatin; thyroid hormones such as calcitonin, calcitonin precursors, and calcitonin gene related peptides; parathyroid hormones and their related proteins; pancreatic hormones such as insulin and insulin-like peptides, glucagon, somatostatin, pancreatic polypeptides, amylin, peptide YY, and neuropeptide Y; digestive hormones such as gastrin, gastrin releasing peptides, gastrin inhibitory peptides, cholecystokinin, secretin, motilin, and vasoactive intestinal peptide; natriuretic peptides such as atrial natriuretic peptides, brain natriuretic peptides, and C-type natriuretic peptides; neurokinins such as neurokinin A, neurokinin B, and substance P; renin related peptides such as renin substrates and inhibitors and angiotensins; endothelins, including big endothelin, endothelin A receptor antagonists, and sarafotoxin peptides; and other peptides such as adrenomedullin peptides, allatostatin peptides, amyloid beta protein fragments, antibiotic and antimicrobial peptides, apoptosis related peptides, bag cell peptides, bombesin, bone Gla protein peptides, CART peptides, chemotactic peptides, cortistatin peptides, fibronectin fragments and fibrin related peptides, FMRF and analog peptides, galanin and related peptides, growth factors and related peptides, G therapeutic peptide-binding protein fragments, guanylin and uroguanylin, inhibin peptides, interleukin and interleukin receptor proteins, laminin fragments, leptin fragment peptides, leucokinins, mast cell degranulating peptides, pituitary adenylate cyclase activating polypeptides, pancreastatin, peptide T, polypeptides, virus related peptides, signal transduction reagents, toxins, and miscellaneous peptides such as adjuvant peptide analogs, alpha mating factor, antiarrhythmic peptide, antifreeze polypeptide, anorexigenic peptide, bovine pineal antireproductive peptide, bursin, C3 peptide P16, tumor necrosis factor, cadherin peptide, chromogranin A

fragment, contraceptive tetrapeptide, conantokin G, conantokin T, crustacean cardioactive peptide, C-telopeptide, cytochrome b588 peptide, decorsin, delicious peptide, delta-sleep-inducing peptide, diazepam-binding inhibitor fragment, nitric oxide synthase blocking peptide, OVA peptide, platelet calpain inhibitor (P1), plasminogen activator inhibitor 1, rigin, schizophrenia related peptide, serum thymic factor, sodium potassium A therapeutic peptidase inhibitor-1, speract, sperm activating peptide, systemin, thrombin receptor agonists, thymic humoral gamma2 factor, thymopentin, thymosin alpha 1, thymus factor, tuftsin, adipo-kinetic hormone, uremic pentapeptide, glucose-dependent insulinotropic polypeptide (GIP), glucagon-like peptide-1 (GLP-1), glucagon-like peptide-2 (GLP-1), exendin-3, exendin-4, and other therapeutic peptides or fragments thereof. Additional examples of peptides include ghrelin, opioid peptides (casomorphin peptides, demorphins, endorphins, enkephalins, deltorphins, dynorphins, and analogs and derivatives of these), thymic peptides (thymopoietin, thymulin, thymopentin, thymosin, Thymic Humoral Factor (THF)), cell adhesion peptides, complement inhibitors, thrombin inhibitors, trypsin inhibitors, alpha-1 antitrypsin, Sea Urchin Sperm Activating Peptide, SHU-9119 MC3-R & MC4-R Antagonist, glaspimod (immunostimulant, useful against bacterial infections, fungal infections, immune deficiency immune disorder, leukopenia), BP-228 (melanocortin, useful against chemotherapy induced emesis, toxicity, pain, diabetes mellitus, inflammation, rheumatoid arthritis, obesity), alpha 2-plasmin inhibitor (plasmin inhibitor), APC tumor suppressor (tumor suppressor, useful against neoplasm), early pregnancy factor (immunosuppressor), endozepine diazepam binding inhibitor (receptor peptide), gamma interferon (useful against leukemia), glandular kallikrein-1 (immunostimulant), placental ribonuclease inhibitor, sarcosol binding protein, surfactant protein D, Wilms' tumor suppressor, GABAB 1b receptor peptide, prion related peptide (iPrP13), choline binding protein fragment (bacterial related peptide), telomerase inhibitor, cardiostatin peptide, endostatin derived peptide (angiogenesis inhibitor), prion inhibiting peptide, N-methyl D-aspartate receptor antagonist, C-peptide analog (useful against diabetic complications), RANTES, NTY receptors, NPY2-R (neuropeptide Y type 2-receptor) ligands, NC4R peptides, or fragments thereof. See U.S. Pat. No. 6,849,714 which is incorporated by reference herein. Also included are Alpha-1 antitrypsin, Angiostatin, Antihemolytic factor, antibodies, Apolipoprotein, Apoprotein, Atrial natriuretic factor, Atrial natriuretic polypeptide, Atrial peptides, C-X-C chemokines (e.g., T39765, NAP-2, ENA-78, Gro-a, Gro-b, Gro-c, IP-10, GCP-2, NAP-4, SDF-1, PF4, MIG), Calcitonin, CC chemokines (e.g., Monocyte chemoattractant protein-1, Monocyte chemoattractant protein-2, Monocyte chemoattractant protein-3, Monocyte inflammatory protein-1 alpha, Monocyte inflammatory protein-1 beta, RANTES, 1309, R83915, R91733, HCC1, T58847, D31065, T64262), CD40 ligand, C-kit Ligand, Collagen, Colony stimulating factor (CSF), Complement factor 5a, Complement inhibitor, Complement receptor 1, cytokines, (e.g., epithelial Neutrophil Activating Peptide-78, GRO/MGSA, GRO, GRO, MIP-1, MIP-1, MCP-1), Epidermal Growth Factor (EGF), Erythropoietin ("EPO"), Exfoliating toxins A and B, Factor IX, Factor VII, Factor VIII, Factor X, Fibroblast Growth Factor (FGF), Fibrinogen, Fibronectin, G-CSF, GM-CSF, Glucocerebrosidase, Gonadotropin, growth factors, Hedgehog proteins (e.g., Sonic, Indian, Desert), Hemoglobin, Hepatocyte Growth Factor (HGF), Hirudin, Human serum albumin, Insulin, Insulin-like Growth Factor (IGF), interferons (e.g., IFN- α , IFN- β , IFN- γ), interleukins (e.g.,

IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, etc.), Keratinocyte Growth Factor (KGF), Lactoferrin, leukemia inhibitory factor, Luciferase, Neur-
trophil inhibitory factor (NIF), oncostatin M, Osteogenic protein, Parathyroid hormone, PD-ECSF, PDGF,
peptide hormones (e.g., Human Growth Hormone), Pleiotro-
pin, Protein A, Protein G, Pyrogenic exotoxins A, B, and C,
Relaxin, Renin, SCF, Soluble complement receptor I, Soluble
I-CAM 1, Soluble interleukin receptors (IL-1, 2, 3, 4, 5, 6, 7,
9, 10, 11, 12, 13, 14, 15), Soluble TNF receptor, Somatome-
din, Somatostatin, Somatotropin, Streptokinase, Superanti-
gens, i.e., Staphylococcal enterotoxins (SEA, SEB, SEC1,
SEC2, SEC3, SED, SEE), Superoxide dismutase, Toxic
shock syndrome toxin (TSST-1), Thymosin alpha 1, Tissue
plasminogen activator, Tumor necrosis factor beta (TNF
beta), Tumor necrosis factor receptor (TNFR), Tumor necro-
sis factor-alpha (TNF alpha), Vascular Endothelial Growth
Factor (VEGFR), Urokinase, T-20, SS-14, LHRH, erythro-
poietin (EPO), G-CSF, TPO, axokine, leptin, and many oth-
ers. Examples of hA conjugated, linked, or fused to biologi-
cally active molecules may be found in U.S. Pat. Nos. 7,056,
701; 7,041,478; 7,045,318; 6,994,857; 6,987,006; 6,972,322;
6,946,134; 6,926,898; 6,905,688; 6,686,179; 6,548,653;
6,423,512; 5,773,417; and 5,594,110, which are incorporated
by reference herein.

A "bifunctional polymer" or "bifunctional linker" refers to
a molecule comprising two discrete functional groups that are
capable of reacting specifically with other moieties (includ-
ing but not limited to, amino acid side groups) to form coval-
ent or non-covalent linkages. A bifunctional linker having
one functional group reactive with a group on a particular
biologically active component, and another group reactive with
a group on a second biological component, may be used
to form a conjugate that includes the first biologically active
component, the bifunctional linker and the second biologi-
cally active component. Many procedures and linker mole-
cules for attachment of various compounds to peptides are
known. See, e.g., European Patent Application No. 188,256;
U.S. Pat. Nos. 4,671,958, 4,659,839, 4,414,148, 4,699,784;
4,680,338; and 4,569,789 which are incorporated by refer-
ence herein. A "multi-functional polymer" or "multi-func-
tional linker" refers to a molecule comprising two or more
discrete functional groups that are capable of reacting spec-
ifically with other moieties (including but not limited to,
amino acid side groups) to form covalent or non-covalent
linkages. A bi-functional polymer or linker, or a multi-func-
tional polymer or linker may be any desired length or molecu-
lar weight, and may be selected to provide a particular desired
spacing or conformation between one or more molecules
linked to the hPP or hFc and its binding partner or the hPP or
hFc.

Where substituent groups are specified by their conven-
tional chemical formulas, written from left to right, they
equally encompass the chemically identical substituents that
would result from writing the structure from right to left, for
example, the structure $\text{—CH}_2\text{O—}$ is equivalent to the struc-
ture $\text{—OCH}_2\text{—}$.

The term "substituents" includes but is not limited to "non-
interfering substituents". "Non-interfering substituents" are
those groups that yield stable compounds. Suitable non-in-
terfering substituents or radicals include, but are not limited
to, halo, $\text{C}_1\text{—C}_{10}$ alkyl, $\text{C}_2\text{—C}_{10}$ alkenyl, $\text{C}_2\text{—C}_{10}$ alkynyl,
 $\text{C}_1\text{—C}_{10}$ alkoxy, $\text{C}_1\text{—C}_{12}$ alkaryl, $\text{C}_1\text{—C}_{12}$ alkaryl, $\text{C}_3\text{—C}_{12}$
cycloalkyl, $\text{C}_3\text{—C}_{12}$ cycloalkenyl, phenyl, substituted phenyl,
toluoyl, xylenyl, biphenyl, $\text{C}_2\text{—C}_{12}$ alkoxyalkyl, $\text{C}_2\text{—C}_{12}$
alkoxyaryl, $\text{C}_7\text{—C}_{12}$ aryloxyalkyl, $\text{C}_7\text{—C}_{12}$ oxyaryl, $\text{C}_1\text{—C}_6$
alkylsulfinyl, $\text{C}_1\text{—C}_{10}$ alkylsulfonyl, $\text{—(CH}_2)_m\text{—O—(C}_1\text{—C}_{10}$

alkyl) wherein m is from 1 to 8, aryl, substituted aryl, substi-
tuted alkoxy, fluoroalkyl, heterocyclic radical, substituted
heterocyclic radical, nitroalkyl, —NO_2 , —CN , —NRC(O)—
 $\text{(C}_1\text{—C}_{10}\text{ alkyl)}$, $\text{—C(O)—(C}_1\text{—C}_{10}\text{ alkyl)}$, $\text{C}_2\text{—C}_{10}$ alkyl thio-
alkyl, $\text{—C(O)O—(C}_1\text{—C}_{10}\text{ alkyl)}$, —OH , —SO_2 , =S ,
 —COOH , —NR_2 , carbonyl, $\text{—C(O)—(C}_1\text{—C}_{10}\text{ alkyl)—CF}_3$,
 —C(O)—CF_3 , —C(O)NR_2 , $\text{—(C}_1\text{—C}_{10}\text{ aryl)—S—(C}_6\text{—C}_{10}$
aryl), $\text{—C(O)—(C}_1\text{—C}_{10}\text{ aryl)}$, $\text{—(CH}_2)_m\text{—O—(—(CH}_2)_m\text{—}$
 $\text{O—(C}_1\text{—C}_{10}\text{ alkyl)}$ wherein each m is from 1 to 8, —C(O)
 NR_2 , —C(S)NR_2 , SO_2NR_2 , —NRC(O)NR_2 , —NRC(S)
 NR_2 , salts thereof, and the like. Each R as used herein is H,
alkyl or substituted alkyl, aryl or substituted aryl, aralkyl, or
alkaryl.

The term "halogen" includes fluorine, chlorine, iodine, and
bromine

The term "alkyl," by itself or as part of another substituent,
means, unless otherwise stated, a straight or branched chain,
or cyclic hydrocarbon radical, or combination thereof, which
may be fully saturated, mono- or polyunsaturated and can
include di- and multivalent radicals, having the number of
carbon atoms designated (i.e. $\text{C}_1\text{—C}_{10}$ means one to ten car-
bons). Examples of saturated hydrocarbon radicals include,
but are not limited to, groups such as methyl, ethyl, n-propyl,
isopropyl, n-butyl, t-butyl, isobutyl, sec-butyl, cyclohexyl,
(cyclohexyl)methyl, cyclopropylmethyl, homologs and iso-
mers of, for example, n-pentyl, n-hexyl, n-heptyl, n-octyl, and
the like. An unsaturated alkyl group is one having one or more
double bonds or triple bonds. Examples of unsaturated alkyl
groups include, but are not limited to, vinyl, 2-propenyl,
crotyl, 2-isopentenyl, 2-(butadienyl), 2,4-pentadienyl, 3-(1,
4-pentadienyl), ethynyl, 1- and 3-propynyl, 3-butylnyl, and
the higher homologs and isomers. The term "alkyl," unless
otherwise noted, is also meant to include those derivatives of
alkyl defined in more detail below, such as "heteroalkyl."
Alkyl groups which are limited to hydrocarbon groups are
termed "homoalkyl".

The term "alkylene" by itself or as part of another substituent
means a divalent radical derived from an alkane, as exem-
plified, but not limited, by the structures $\text{—CH}_2\text{CH}_2\text{—}$ and
 $\text{—CH}_2\text{CH}_2\text{CH}_2\text{CH}_2\text{—}$, and further includes those groups
described below as "heteroalkylene." Typically, an alkyl (or
alkylene) group will have from 1 to 24 carbon atoms, with
those groups having 10 or fewer carbon atoms being a particu-
lar embodiment of the methods and compositions
described herein. A "lower allyl" or "lower alkylene" is a
shorter chain alkyl or alkylene group, generally having eight
or fewer carbon atoms.

The terms "alkoxy," "alkylamino" and "alkylthio" (or thio-
alkoxy) are used in their conventional sense, and refer to those
alkyl groups attached to the remainder of the molecule via an
oxygen atom, an amino group, or a sulfur atom, respectively.

The term "heteroalkyl," by itself or in combination with
another term, means, unless otherwise stated, a stable straight
or branched chain, or cyclic hydrocarbon radical, or combi-
nations thereof, consisting of the stated number of carbon
atoms and at least one heteroatom selected from the group
consisting of O, N, Si and S, and wherein the nitrogen and
sulfur atoms may optionally be oxidized and the nitrogen
heteroatom may optionally be quaternized. The hetero-
atom(s) O, N and S and Si may be placed at any interior
position of the heteroalkyl group or at the position at which
the alkyl group is attached to the remainder of the molecule.
Examples include, but are not limited to, $\text{—CH}_2\text{—CH}_2\text{—}$
 O—CH_3 , $\text{—CH}_2\text{—CH}_2\text{—NH—CH}_3$, $\text{—CH}_2\text{—CH}_2\text{—N}$
 $\text{(CH}_3\text{)—CH}_3$, $\text{—CH}_2\text{—S—CH}_2\text{—CH}_3$, $\text{—CH}_2\text{—CH}_2\text{—}$
 S(O)—CH_3 , $\text{—CH}_2\text{—CH}_2\text{—S(O)}_2\text{—CH}_3$, —CH=CH—
 O—CH_3 , $\text{—Si(CH}_3\text{)}_3$, $\text{—CH}_2\text{—CH=N—OCH}_3$, and

—CH=CH—N(CH₃)—CH₃. Up to two heteroatoms may be consecutive, such as, for example, —CH₂—NH—OCH₃ and —CH₂—O—Si(CH₃)₃. Similarly, the term “heteroalkylene” by itself or as part of another substituent means a divalent radical derived from heteroalkyl, as exemplified, but not limited by, —CH₂—CH₂—S—CH₂—CH₂— and —CH₂—S—CH₂—CH₂—NH—C₁₋₁₂—. For heteroalkylene groups, the same or different heteroatoms can also occupy either or both of the chain termini (including but not limited to, alkyleneoxy, alkyleneedioxy, alkyleneamino, alkyleneamino, aminoxyalkylene, and the like). Still further, for alkylene and heteroalkylene linking groups, no orientation of the linking group is implied by the direction in which the formula of the linking group is written. For example, the formula —C(O)₂R'— represents both —C(O)₂R'— and —R'C(O)₂—.

The terms “cycloalkyl” and “heterocycloalkyl”, by themselves or in combination with other terms, represent, unless otherwise stated, cyclic versions of “alkyl” and “heteroalkyl”, respectively. Thus, a cycloalkyl or heterocycloalkyl include saturated, partially unsaturated and fully unsaturated ring linkages. Additionally, for heterocycloalkyl, a heteroatom can occupy the position at which the heterocycle is attached to the remainder of the molecule. Examples of cycloalkyl include, but are not limited to, cyclopentyl, cyclohexyl, 1-cyclohexenyl, 3-cyclohexenyl, cycloheptyl, and the like. Examples of heterocycloalkyl include, but are not limited to, 1-(1,2,5,6-tetrahydropyridyl), 1-piperidiny, 2-piperidiny, 3-piperidiny, 4-morpholinyl, 3-morpholinyl, tetrahydrofuran-2-yl, tetrahydrofuran-3-yl, tetrahydrothien-2-yl, tetrahydrothien-3-yl, 1-piperazinyl, 2-piperazinyl, and the like. Additionally, the term encompasses bicyclic and tricyclic ring structures. Similarly, the term “heterocycloalkylene” by itself or as part of another substituent means a divalent radical derived from heterocycloalkyl, and the term “cycloalkylene” by itself or as part of another substituent means a divalent radical derived from cycloalkyl.

As used herein, the term “water soluble polymer” refers to any polymer that is soluble in aqueous solvents. Linkage of water soluble polymers to hPP or hA or hFc polypeptides can result in changes including, but not limited to, increased or modulated serum half-life, or increased or modulated therapeutic half-life relative to the unmodified form, modulated immunogenicity, modulated physical association characteristics such as aggregation and multimer formation, altered receptor binding, altered binding to one or more binding partners, and altered receptor dimerization or multimerization. The water soluble polymer may or may not have its own biological activity, and may be utilized as a linker for attaching hPP or hA or hFc to other substances, including but not limited to one or more hPP or hA or hFc polypeptides, or one or more biologically active molecules. Suitable polymers include, but are not limited to, polyethylene glycol, polyethylene glycol propionaldehyde, mono C₁-C₁₀ alkoxy or aryloxy derivatives thereof (described in U.S. Pat. No. 5,252,714 which is incorporated by reference herein), monomethoxy-polyethylene glycol, polyvinyl pyrrolidone, polyvinyl alcohol, polyamino acids, divinylether maleic anhydride, N-(2-Hydroxypropyl)-methacrylamide, dextran, dextran derivatives including dextran sulfate, polypropylene glycol, polypropylene oxide/ethylene oxide copolymer, polyoxyethylated polyol, heparin, heparin fragments, polysaccharides, oligosaccharides, glycans, cellulose and cellulose derivatives, including but not limited to methylcellulose and carboxymethyl cellulose, starch and starch derivatives, polypeptides, polyalkylene glycol and derivatives thereof, copolymers of polyalkylene glycols and derivatives thereof,

polyvinyl ethyl ethers, and alpha-beta-poly[(2-hydroxyethyl)-DL-aspartamide, and the like, or mixtures thereof. Examples of such water soluble polymers include, but are not limited to, polyethylene glycol and serum albumin.

As used herein, the term “polyalkylene glycol” or “poly(alkene glycol)” refers to polyethylene glycol (poly(ethylene glycol)), polypropylene glycol, polybutylene glycol, and derivatives thereof. The term “polyalkylene glycol” encompasses both linear and branched polymers and average molecular weights of between 0.1 kDa and 100 kDa. Other exemplary embodiments are listed, for example, in commercial supplier catalogs, such as Shearwater Corporation’s catalog “Polyethylene Glycol and Derivatives for Biomedical Applications” (2001).

The term “aryl” means, unless otherwise stated, a polyunsaturated, aromatic, hydrocarbon substituent which can be a single ring or multiple rings (including but not limited to, from 1 to 3 rings) which are fused together or linked covalently. The term “heteroaryl” refers to aryl groups (or rings) that contain from one to four heteroatoms selected from N, O, and S, wherein the nitrogen and sulfur atoms are optionally oxidized, and the nitrogen atom(s) are optionally quaternized. A heteroaryl group can be attached to the remainder of the molecule through a heteroatom. Non-limiting examples of aryl and heteroaryl groups include phenyl, 1-naphthyl, 2-naphthyl, 4-biphenyl, 1-pyrrolyl, 2-pyrrolyl, 3-pyrrolyl, 3-pyrazolyl, 2-imidazolyl, 4-imidazolyl, pyrazinyl, 2-oxazolyl, 4-oxazolyl, 2-phenyl-4-oxazolyl, 5-oxazolyl, 3-isoxazolyl, 4-isoxazolyl, 5-isoxazolyl, 2-thiazolyl, 4-thiazolyl, 5-thiazolyl, 2-furyl, 3-furyl, 2-thienyl, 3-thienyl, 2-pyridyl, 3-pyridyl, 4-pyridyl, 2-pyrimidyl, 5-benzothiazolyl, purinyl, 2-benzimidazolyl, 5-indolyl, 1-isoquinolyl, 5-isoquinolyl, 2-quinoxalyl, 5-quinoxalyl, 3-quinolyl, and 6-quinolyl. Substituents for each of the above noted aryl and heteroaryl ring systems are selected from the group of acceptable substituents described below.

For brevity, the term “aryl” when used in combination with other terms (including but not limited to, aryloxy, arylthioxy, arylalkyl) includes both aryl and heteroaryl rings as defined above. Thus, the term “arylalkyl” is meant to include those radicals in which an aryl group is attached to an alkyl group (including but not limited to, benzyl, phenethyl, pyridylmethyl and the like) including those alkyl groups in which a carbon atom (including but not limited to, a methylene group) has been replaced by, for example, an oxygen atom (including but not limited to, phenoxymethyl, 2-pyridyloxymethyl, 3-(1-naphthyloxy)propyl, and the like).

Each of the above terms (including but not limited to, “alkyl,” “heteroalkyl,” “aryl” and “heteroaryl”) are meant to include both substituted and unsubstituted forms of the indicated radical. Exemplary substituents for each type of radical are provided below.

Substituents for the alkyl and heteroalkyl radicals (including those groups often referred to as alkylene, alkenyl, heteroalkylene, heteroalkenyl, alkynyl, cycloalkyl, heterocycloalkyl, cycloalkenyl, and heterocycloalkenyl) can be one or more of a variety of groups selected from, but not limited to: —OR', —O, —NR', —N—OR', —NR'R'', —SR', —halogen, —SiR'R''R''', —OC(O)R', —C(O)R', —CO₂R', —CONR'R'', —OC(O)NR'R'', —NR'C(O)R', —NR'—C(O)NR'R'', —NR'C(O)₂R', —NR—C(NR'R''R''')=NR''', —NR—C(NR'R'')=NR''', —S(O)R', —S(O)₂R', —S(O)₂NR'R'', —NRSO₂R', —CN and —NO₂ in a number ranging from zero to (2 m'+1), where m' is the total number of carbon atoms in such a radical. R', R'', R''' and R'''' each independently refer to hydrogen, substituted or unsubstituted heteroalkyl, substituted or unsubstituted aryl, including but

not limited to, aryl substituted with 1-3 halogens, substituted or unsubstituted alkyl, alkoxy or thioalkoxy groups, or arylalkyl groups. When a compound of the invention includes more than one R group, for example, each of the R groups is independently selected as are each R', R'', R''' and R'''' groups when more than one of these groups is present. When R' and R'' are attached to the same nitrogen atom, they can be combined with the nitrogen atom to form a 5-, 6-, or 7-membered ring. For example, —NR'R'' is meant to include, but not be limited to, 1-pyrrolidinyl and 4-morpholinyl. From the above discussion of substituents, one of skill in the art will understand that the term “alkyl” is meant to include groups including carbon atoms bound to groups other than hydrogen groups, such as haloalkyl (including but not limited to, —CF₃ and —CH₂CF₃) and acyl (including but not limited to, —C(O)CH₃, —C(O)CF₃, —C(O)CH₂OCH₃, and the like).

Similar to the substituents described for the alkyl radical, substituents for the aryl and heteroaryl groups are varied and are selected from, but are not limited to: halogen, —OR', —O, —NR', —N—OR', —NR'R'', —SR', —halogen, —SiR'R''R''', —OC(O)R', —C(O)R', —CO₂R', —CONR'R'', —OC(O)NR'R'', —NR''C(O)R', —NR''C(O)NR''R''', —NR''C(O)₂R', —NR—C(NR'R''R''')=NR''', —NR—C(NR'R''R''')=NR''', —S(O)R', —S(O)₂R', —S(O)₂NR'R'', —NRSO₂R', —CN and —NO₂, —R', —N₃, —CH(Ph)₂, fluoro(C₁-C₄)alkoxy, and fluoro(C₁-C₄)alkyl, in a number ranging from zero to the total number of open valences on the aromatic ring system; and where R', R'', R''' and R'''' are independently selected from hydrogen, alkyl, heteroalkyl, aryl and heteroaryl. When a compound of the invention includes more than one R group, for example, each of the R groups is independently selected as are each R', R'', R''' and R'''' groups when more than one of these groups is present.

As used herein, the term “modulated serum half-life” means the positive or negative change in circulating half-life of a modified hPP or hA or hFc relative to its non-modified form. Serum half-life is measured by taking blood samples at various time points after administration of hPP or hA or hFc, and determining the concentration of that molecule in each sample. Correlation of the serum concentration with time allows calculation of the serum half-life. Increased serum half-life desirably has at least about two-fold, but a smaller increase may be useful, for example where it enables a satisfactory dosing regimen or avoids a toxic effect. In some embodiments, the increase is at least about three-fold, at least about five-fold, or at least about ten-fold.

The term “modulated therapeutic half-life” as used herein means the positive or negative change in the half-life of the therapeutically effective amount of hPP or hA or hFc, relative to its non-modified form. Therapeutic half-life is measured by measuring pharmacokinetic and/or pharmacodynamic properties of the molecule at various time points after administration. Increased therapeutic half-life desirably enables a particular beneficial dosing regimen, a particular beneficial total dose, or avoids an undesired effect. In some embodiments, the increased therapeutic half-life results from increased potency, increased or decreased binding of the modified molecule to its target, increased or decreased breakdown of the molecule by enzymes such as proteases, or an increase or decrease in another parameter or mechanism of action of the non-modified molecule.

The term “isolated,” when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is free of at least some of the cellular components with which it is associated in the natural state, or that the nucleic acid or protein has been concentrated to a level greater than the concentration of its in vivo or in vitro production. It can be in a homo-

neous state. Isolated substances can be in either a dry or semi-dry state, or in solution, including but not limited to, an aqueous solution. It can be a component of a pharmaceutical composition that comprises additional pharmaceutically acceptable carriers and/or excipients. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein which is the predominant species present in a preparation is substantially purified. In particular, an isolated gene is separated from open reading frames which flank the gene and encode a protein other than the gene of interest. The term “purified” denotes that a nucleic acid or protein gives rise to substantially one band in an electrophoretic gel. Particularly, it may mean that the nucleic acid or protein is at least 85% pure, at least 90% pure, at least 95% pure, at least 99% or greater pure.

The term “nucleic acid” refers to deoxyribonucleotides, deoxyribonucleosides, ribonucleosides, or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless specifically limited otherwise, the term also refers to oligonucleotide analogs including PNA (peptidonucleic acid), analogs of DNA used in antisense technology (phosphorothioates, phosphoroamidates, and the like). Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (including but not limited to, degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al., *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka et al., *J. Biol. Chem.* 260:2605-2608 (1985); Rossolini et al., *Mol. Cell. Probes* 8:91-98 (1994)).

The terms “polypeptide,” “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. That is, a description directed to a polypeptide applies equally to a description of a peptide and a description of a protein, and vice versa. The terms apply to naturally occurring amino acid polymers as well as amino acid polymers in which one or more amino acid residues is a non-naturally encoded amino acid. As used herein, the terms encompass amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds.

The term “amino acid” refers to naturally occurring and non-naturally occurring amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally encoded amino acids are the 20 common amino acids (alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine) and pyrrolysine and selenocysteine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, such as, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (such as, norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, "conservatively modified variants" refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of ordinary skill in the art will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

As to amino acid sequences, one of ordinary skill in the art will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the deletion of an amino acid, addition of an amino acid, or substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are known to those of ordinary skill in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

Conservative substitution tables providing functionally similar amino acids are known to those of ordinary skill in the art. The following eight groups each contain amino acids that are conservative substitutions for one another:

- 1) Alanine (A), Glycine (G);
- 2) Aspartic acid (D), Glutamic acid (E);
- 3) Asparagine (N), Glutamine (Q);
- 4) Arginine (R), Lysine (K);
- 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V);
- 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W);
- 7) Serine (S), Threonine (T); and
- 8) Cysteine (C), Methionine (M)

(see, e.g., *Creighton, Proteins: Structures and Molecular Properties* (W H Freeman & Co.; 2nd edition (December 1993))

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same. Sequences are "substantially identical" if they have a percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95% identity over a specified region), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following

sequence comparison algorithms (or other algorithms available to persons of ordinary skill in the art) or by manual alignment and visual inspection. This definition also refers to the complement of a test sequence. The identity can exist over a region that is at least about 50 amino acids or nucleotides in length, or over a region that is 75-100 amino acids or nucleotides in length, or, where not specified, across the entire sequence of a polynucleotide or polypeptide.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are known to those of ordinary skill in the art. Optimal alignment of sequences for comparison can be conducted, including but not limited to, by the local homology algorithm of Smith and Waterman (1970) *Adv. Appl. Math.* 2:482c, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988) *Proc. Nat'l. Acad. Sci. USA* 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, PASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by manual alignment and visual inspection (see, e.g., Ausubel et al., *Current Protocols in Molecular Biology* (1995 supplement)).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1997) *Nuc. Acids Res.* 25:3389-3402, and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information available at the World Wide Web at ncbi.nlm.nih.gov. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands. The BLAST algorithm is typically performed with the "low complexity" filter turned off.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance.

For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, or less than about 0.01, or less than about 0.001.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (including but not limited to, total cellular or library DNA or RNA).

The phrase “stringent hybridization conditions” refers to hybridization of sequences of DNA, RNA, PNA, or other nucleic acid mimics, or combinations thereof under conditions of low ionic strength and high temperature as is known in the art. Typically, under stringent conditions a probe will hybridize to its target subsequence in a complex mixture of nucleic acid (including but not limited to, total cellular or library DNA or RNA) but does not hybridize to other sequences in the complex mixture. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Probes*, “Overview of principles of hybridization and the strategy of nucleic acid assays” (1993). Generally, stringent conditions are selected to be about 5-10° C. lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions may be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (including but not limited to, 10 to 50 nucleotides) and at least about 60° C. for long probes (including but not limited to, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal may be at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5×SSC, and 1% SDS, incubating at 42° C., or 5×SSC, 1% SDS, incubating at 65° C., with wash in 0.2×SSC, and 0.1% SDS at 65° C. Such washes can be performed for 5, 15, 30, 60, 120, or more minutes.

As used herein, the term “eukaryote” refers to organisms belonging to the phylogenetic domain Eucarya such as animals (including but not limited to, mammals, insects, reptiles, birds, etc.), ciliates, plants (including but not limited to, monocots, dicots, algae, etc.), fungi, yeasts, flagellates, microsporidia, protists, etc.

As used herein, the term “non-eukaryote” refers to non-eukaryotic organisms. For example, a non-eukaryotic organism can belong to the Eubacteria (including but not limited to, *Escherichia coli*, *Thermus thermophilus*, *Bacillus stearothermophilus*, *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, etc.) phylogenetic domain, or the Archaea (including but not limited to, *Methanococcus jannaschii*, *Methanobacterium thermoautotrophicum*, *Halobacterium* such as *Haloferax volcanii* and *Halobacterium* species NRC-1, *Archaeoglobus fulgidus*, *Pyrococcus furiosus*, *Pyrococcus horikoshii*, *Aeuryopyrum pernix*, etc.) phylogenetic domain.

The term “subject” as used herein, refers to an animal, in some embodiments a mammal, and in other embodiments a human, who is the object of treatment, observation or experiment.

The term “effective amount” as used herein refers to that amount of the modified non-natural amino acid polypeptide being administered which will relieve to some extent one or more of the symptoms of the disease, condition or disorder being treated. Compositions containing the modified non-natural amino acid polypeptide described herein can be administered for prophylactic, enhancing, and/or therapeutic treatments.

The terms “enhance” or “enhancing” means to increase or prolong either in potency or duration a desired effect. Thus, in regard to enhancing the effect of therapeutic agents, the term “enhancing” refers to the ability to increase or prolong, either in potency or duration, the effect of other therapeutic agents on a system. An “enhancing-effective amount,” as used herein, refers to an amount adequate to enhance the effect of another therapeutic agent in a desired system. When used in a patient, amounts effective for this use will depend on the severity and course of the disease, disorder or condition, previous therapy, the patient’s health status and response to the drugs, and the judgment of the treating physician.

The term “modified,” as used herein refers to any changes made to a given polypeptide, such as changes to the length of the polypeptide, the amino acid sequence, chemical structure, co-translational modification, or post-translational modification of a polypeptide. The form “(modified)” term means that the polypeptides being discussed are optionally modified, that is, the polypeptides under discussion can be modified or unmodified.

The term “post-translationally modified” refers to any modification of a natural or non-natural amino acid that occurs to such an amino acid after it has been incorporated into a polypeptide chain. The term encompasses, by way of example only, co-translational in vivo modifications, co-translational in vitro modifications (such as in a cell-free translation system), post-translational in vivo modifications, and post-translational in vitro modifications.

In prophylactic applications, compositions containing the modified non-natural amino acid polypeptide are administered to a patient susceptible to or otherwise at risk of a particular disease, disorder or condition. Such an amount is defined to be a “prophylactically effective amount.” In this use, the precise amounts also depend on the patient’s state of health, weight, and the like. It is considered well within the skill of the art for one to determine such prophylactically effective amounts by routine experimentation (e.g., a dose escalation clinical trial).

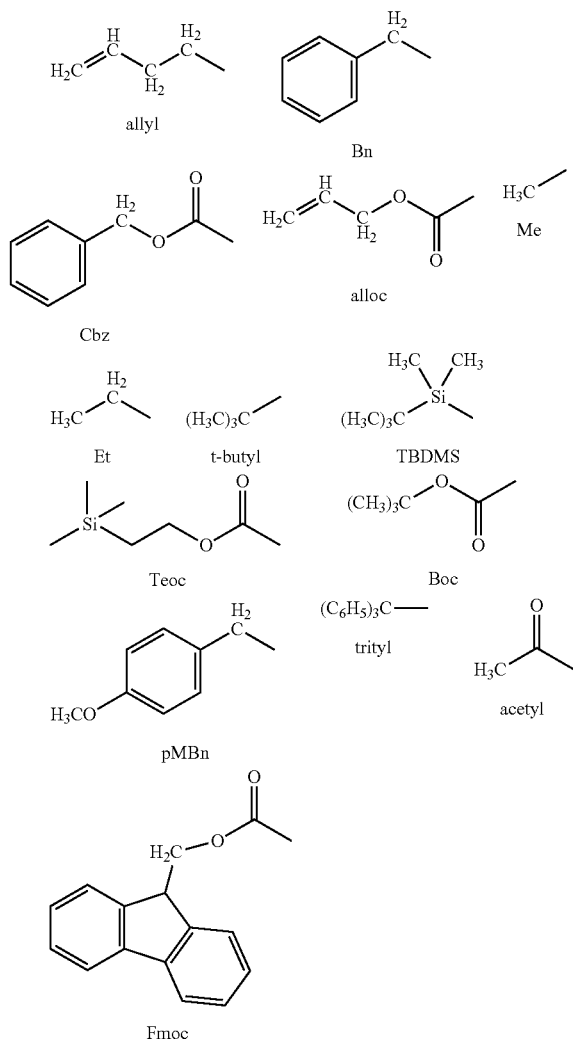
The term “protected” refers to the presence of a “protecting group” or moiety that prevents reaction of the chemically reactive functional group under certain reaction conditions.

The protecting group will vary depending on the type of chemically reactive group being protected. For example, if the chemically reactive group is an amine or a hydrazide, the protecting group can be selected from the group of tert-butyloxycarbonyl (t-Boc) and 9-fluorenylmethoxycarbonyl (Fmoc). If the chemically reactive group is a thiol, the protecting group can be orthopyridyldisulfide. If the chemically reactive group is a carboxylic acid, such as butanoic or propionic acid, or a hydroxyl group, the protecting group can be benzyl or an alkyl group such as methyl, ethyl, or tert-butyl. Other protecting groups known in the art may also be used in or with the methods and compositions described herein, including photolabile groups such as Nvoc and MeNvoc.

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Other protecting groups known in the art may also be used in or with the methods and compositions described herein.

By way of example only, blocking/protecting groups may be selected from:



Other protecting groups are described in Greene and Wuts, *Protective Groups in Organic Synthesis*, 3rd Ed., John Wiley & Sons, New York, N.Y., 1999, which is incorporated herein by reference in its entirety.

In therapeutic applications, compositions containing the modified non-natural amino acid polypeptide are administered to a patient already suffering from a disease, condition or disorder, in an amount sufficient to cure or at least partially arrest the symptoms of the disease, disorder or condition. Such an amount is defined to be a "therapeutically effective amount," and will depend on the severity and course of the disease, disorder or condition, previous therapy, the patient's health status and response to the drugs, and the judgment of the treating physician. It is considered well within the skill of the art for one to determine such therapeutically effective amounts by routine experimentation (e.g., a dose escalation clinical trial).

The term "treating" is used to refer to either prophylactic and/or therapeutic treatments.

Non-naturally encoded amino acid polypeptides presented herein may include isotopically-labelled compounds with

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one or more atoms replaced by an atom having an atomic mass or mass number different from the atomic mass or mass number usually found in nature. Examples of isotopes that can be incorporated into the present compounds include isotopes of hydrogen, carbon, nitrogen, oxygen, fluorine and chlorine, such as ^2H , ^3H , ^{13}C , ^{14}C , ^{15}N , ^{18}O , ^{17}O , ^{35}S , ^{18}F , ^{36}Cl , respectively. Certain isotopically-labelled compounds described herein, for example those into which radioactive isotopes such as ^3H and ^{14}C are incorporated, may be useful in drug and/or substrate tissue distribution assays. Further, substitution with isotopes such as deuterium, i.e., ^2H , can afford certain therapeutic advantages resulting from greater metabolic stability, for example increased in vivo half-life or reduced dosage requirements.

All isomers including but not limited to diastereomers, enantiomers, and mixtures thereof are considered as part of the compositions described herein. In additional or further embodiments, the non-naturally encoded amino acid polypeptides are metabolized upon administration to an organism in need to produce a metabolite that is then used to produce a desired effect, including a desired therapeutic effect. In further or additional embodiments are active metabolites of non-naturally encoded amino acid polypeptides.

In some situations, non-naturally encoded amino acid polypeptides may exist as tautomers. In addition, the non-naturally encoded amino acid polypeptides described herein can exist in unsolvated as well as solvated forms with pharmaceutically acceptable solvents such as water, ethanol, and the like. The solvated forms are also considered to be disclosed herein. Those of ordinary skill in the art will recognize that some of the compounds herein can exist in several tautomeric forms. All such tautomeric forms are considered as part of the compositions described herein.

Unless otherwise indicated, conventional methods of mass spectroscopy, NMR, HPLC, protein chemistry, biochemistry, recombinant DNA techniques and pharmacology, within the skill of the art are employed.

DETAILED DESCRIPTION

I. Introduction

The hPP or hFc molecules comprising at least one unnatural amino acid are provided in the present invention. In certain embodiments of the invention, the hPP or hFc polypeptide with at least one unnatural amino acid includes at least one post-translational modification. In some embodiments the hPP is hA. In one embodiment, the at least one post-translational modification of the hPP or hA or hFc comprises attachment of a molecule including but not limited to, a label, a dye, a polymer, a water-soluble polymer, a derivative of polyethylene glycol, a photocrosslinker, a radionuclide, a cytotoxic compound, a drug, an affinity label, a photoaffinity label, a reactive compound, a resin, a second protein or polypeptide or polypeptide analog, an antibody or antibody fragment, a metal chelator, a cofactor, a fatty acid, a carbohydrate, a polynucleotide, a DNA, a RNA, an antisense polynucleotide, a saccharide, a water-soluble dendrimer, a cyclodextrin, an inhibitory ribonucleic acid, a biomaterial, a nanoparticle, a spin label, a fluorophore, a metal-containing moiety, a radioactive moiety, a novel functional group, a group that covalently or noncovalently interacts with other molecules, a photocaged moiety, an actinic radiation excitable moiety, a photoisomerizable moiety, biotin, a derivative of biotin, a biotin analogue, a moiety incorporating a heavy atom, a chemically cleavable group, a photocleavable group, an elongated side chain, a carbon-linked sugar, a redox-active agent,

an amino thioacid, a toxic moiety, an isotopically labeled moiety, a biophysical probe, a phosphorescent group, a chemiluminescent group, an electron dense group, a magnetic group, an intercalating group, a chromophore, an energy transfer agent, a biologically active agent, a detectable label, a small molecule, a quantum dot, a nanotransmitter, a radionucleotide, a radiotransmitter, a neutron-capture agent, or any combination of the above or any other desirable compound or substance, comprising a second reactive group to at least one unnatural amino acid comprising a first reactive group utilizing chemistry methodology that is known to one of ordinary skill in the art to be suitable for the particular reactive groups. For example, the first reactive group is an alkynyl moiety (including but not limited to, in the unnatural amino acid p-propargyloxyphenylalanine, where the propargyl group is also sometimes referred to as an acetylene moiety) and the second reactive group is an azido moiety, and [3+2] cycloaddition chemistry methodologies are utilized. In another example, the first reactive group is the azido moiety (including but not limited to, in the unnatural amino acid p-azido-L-phenylalanine) and the second reactive group is the alkynyl moiety. In certain embodiments of the modified hPP or hA or hFc polypeptide of the present invention, at least one unnatural amino acid (including but not limited to, unnatural amino acid containing a keto functional group) comprising at least one post-translational modification, is used where the at least one post-translational modification comprises a saccharide moiety. In certain embodiments, the post-translational modification is made in vivo in a eukaryotic cell or in a non-eukaryotic cell. A linker, polymer, water soluble polymer, or other molecule may attach the molecule to the polypeptide. The molecule may be linked directly to the polypeptide.

In certain embodiments, the protein includes at least one post-translational modification that is made in vivo by one host cell, where the post-translational modification is not normally made by another host cell type. In certain embodiments, the protein includes at least one post-translational modification that is made in vivo by a eukaryotic cell, where the post-translational modification is not normally made by a non-eukaryotic cell. Examples of post-translational modifications include, but are not limited to, glycosylation, acetylation, acylation, lipid-modification, palmitoylation, palmitate addition, phosphorylation, glycolipid-linkage modification, and the like. In one embodiment, the post-translational modification comprises attachment of an oligosaccharide to an asparagine by a GlcNAc-asparagine linkage (including but not limited to, where the oligosaccharide comprises (GlcNAc-Man)₂-Man-GlcNAc-GlcNAc, and the like). In another embodiment, the post-translational modification comprises attachment of an oligosaccharide (including but not limited to, Gal-GalNAc, Gal-GlcNAc, etc.) to a serine or threonine by a GalNAc-serine, a GalNAc-threonine, a GlcNAc-serine, or a GlcNAc-threonine linkage. In certain embodiments, a protein or polypeptide of the invention can comprise a secretion or localization sequence, an epitope tag, a FLAG tag, a polyhistidine tag, a GST fusion, and/or the like. Examples of secretion signal sequences include, but are not limited to, a prokaryotic secretion signal sequence, a eukaryotic secretion signal sequence, a eukaryotic secretion signal sequence 5'-optimized for bacterial expression, a novel secretion signal sequence, pectate lyase secretion signal sequence, Orly A secretion signal sequence, and a phage secretion signal sequence. Examples of secretion signal sequences, include, but are not limited to, STII (prokaryotic), Fd GIII and M13 (phage), Bgl2 (yeast), and the signal sequence bla derived from a transposon.

The protein or polypeptide of interest can contain at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or ten or more unnatural amino acids. The unnatural amino acids can be the same or different, for example, there can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more different sites in the protein that comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more different unnatural amino acids. In certain embodiments, at least one, but fewer than all, of a particular amino acid present in a naturally occurring version of the protein is substituted with an unnatural amino acid.

The present invention provides methods and compositions based on members of the hPP family, in particular hA, or hFc comprising at least one non-naturally encoded amino acid. Introduction of at least one non-naturally encoded amino acid into an hPP or hA or hFc family member can allow for the application of conjugation chemistries that involve specific chemical reactions, including, but not limited to, with one or more non-naturally encoded amino acids while not reacting with the commonly occurring 20 amino acids. In some embodiments, the hPP or hA or hFc family member comprising the non-naturally encoded amino acid is linked to a water soluble polymer, such as polyethylene glycol (PEG), via the side chain of the non-naturally encoded amino acid. This invention provides a highly efficient method for the selective modification of proteins by coupling the protein with other molecules including but not limited to polymers, linkers, or biologically active molecules, which involves the selective incorporation of non-genetically encoded amino acids, including but not limited to, those amino acids containing functional groups or substituents not found in the 20 naturally incorporated amino acids, including but not limited to a ketone, an azide or acetylene moiety, into proteins in response to a selector codon and the subsequent modification of those amino acids with a suitably reactive molecule. Once incorporated, the amino acid side chains can then be modified by utilizing chemistry methodologies known to those of ordinary skill in the art to be suitable for the particular functional groups or substituents present in the non-naturally encoded amino acid. Known chemistry methodologies of a wide variety are suitable for use in the present invention to couple molecules to the protein. Such methodologies include but are not limited to a Huisgen [3+2] cycloaddition reaction (see, e.g., Padwa, A. in *Comprehensive Organic Synthesis*, Vol. 4, (1991) Ed. Trost, B. M., Pergamon, Oxford, p. 1069-1109; and, Huisgen, R. in *1,3-Dipolar Cycloaddition Chemistry*, (1984) Ed. Padwa, A., Wiley, New York, p. 1-176) with, including but not limited to, acetylene or azide derivatives, respectively.

The present invention provides conjugates of substances having a wide variety of functional groups, substituents or moieties, with other substances including but not limited to a label; a dye; a polymer; a water-soluble polymer; a derivative of polyethylene glycol; a photocrosslinker; a radionuclide; a cytotoxic compound; a drug; an affinity label; a photoaffinity label; a reactive compound; a resin; a second protein or polypeptide or polypeptide analog; an antibody or antibody fragment; a metal chelator; a cofactor; a fatty acid; a carbohydrate; a polynucleotide; a DNA; a RNA; an antisense polynucleotide; a saccharide; a water-soluble dendrimer; a cyclodextrin; an inhibitory ribonucleic acid; a biomaterial; a nanoparticle; a spin label; a fluorophore, a metal-containing moiety; a radioactive moiety; a novel functional group; a group that covalently or noncovalently interacts with other molecules; a photocaged moiety; an actinic radiation excitable moiety; a photoisomerizable moiety; biotin; a derivative of biotin; a biotin analogue; a moiety incorporating a heavy

atom; a chemically cleavable group; a photocleavable group; an elongated side chain; a carbon-linked sugar; a redox-active agent; an amino thioacid; a toxic moiety; an isotopically labeled moiety; a biophysical probe; a phosphorescent group; a chemiluminescent group; an electron dense group; a magnetic group; an intercalating group; a chromophore; an energy transfer agent; a biologically active agent; a detectable label; a small molecule; a quantum dot; a nanotransmitter; a radionucleotide; a radiotransmitter; a neutron-capture agent; or any combination of the above, or any other desirable compound or substance. The present invention also includes conjugates of substances having azide or acetylene moieties with PEG polymer derivatives having the corresponding acetylene or azide moieties. For example, a PEG polymer containing an azide moiety can be coupled to a biologically active molecule at a position in the protein that contains a non-genetically encoded amino acid bearing an acetylene functionality. The linkage by which the PEG and the biologically active molecule are coupled includes but is not limited to the Huisgen [3+2] cycloaddition product.

II. Human Plasma Protein Family

As used herein, "human plasma protein or polypeptide" or "hPP" includes those polypeptides and proteins that are found in normal human blood plasma, including hPP analogs, hPP isoforms, hPP mimetics, hPP fragments, hybrid hPP proteins, fusion proteins, oligomers and multimers, homologues, glycosylation pattern variants, variants, splice variants, and muteins, thereof, regardless of the biological activity of same, and further regardless of the method of synthesis or manufacture thereof including, but not limited to, recombinant (whether produced from cDNA, genomic DNA, synthetic DNA or other form of nucleic acid), in vitro, in vivo, by microinjection of nucleic acid molecules, synthetic, transgenic, and gene activated methods. A variety of hPP's are known in the art and can be found in Anderson et al., *Molecular & Cellular Proteomics*, 3:4:311-326 (2004); and Ping et al., *Proteomics*, 5:3506-3519 (2005), which are incorporated by reference herein.

Additional members of the hPP family are likely to be discovered in the future. New members of the hPP family can be identified through computer-aided secondary and tertiary structure analyses of the predicted protein sequences, and by selection techniques designed to identify molecules that bind to a particular target. Members of the hPP supergene family typically possess four or five amphipathic helices joined by non-helical amino acids (the loop regions). The proteins may contain a hydrophobic signal sequence at their N-terminus to promote secretion from the cell. Such later discovered members of the hPP supergene family also are included within this invention.

Thus, the description of the hPP family or hA is provided for illustrative purposes and by way of example only and not as a limit on the scope of the methods, compositions, strategies and techniques described herein. Further, reference to hPP or hA polypeptides in this application is intended to use the generic term as an example of any member of the hPP family. Thus, it is understood that the modifications and chemistries described herein with reference to hPP or hA polypeptides or protein can be equally applied to any member of the hPP family, including those specifically listed herein.

III. General Recombinant Nucleic Acid Methods for Use with the Invention

In numerous embodiments of the present invention, nucleic acids encoding an hPP polypeptide of interest will be isolated, cloned and often altered using recombinant methods. Such embodiments are used, including but not limited to, for protein expression or during the generation of variants,

derivatives, expression cassettes, or other sequences derived from an hPP or hFc polypeptide. In some embodiments, the sequences encoding the polypeptides of the invention are operably linked to a heterologous promoter. Isolation of hPP and production of hPP in host cells are described in, e.g., U.S. Pat. Nos. 5,648,243; 5,707,828 and 5,521,287, which are incorporated by reference herein.

A nucleotide sequence encoding an hPP polypeptide comprising a non-naturally encoded amino acid may be synthesized on the basis of the amino acid sequence of the parent polypeptide, including but not limited to, having the amino acid sequence shown in SEQ ID NO: 1 and then changing the nucleotide sequence so as to effect introduction (i.e., incorporation or substitution) or removal (i.e., deletion or substitution) of the relevant amino acid residue(s). A nucleotide sequence encoding an hFc polypeptide comprising a non-naturally encoded amino acid may be synthesized on the basis of the amino acid sequence of the parent polypeptide, including but not limited to, having the amino acid sequence shown in SEQ ID NO: 22 and then changing the nucleotide sequence so as to effect introduction (i.e., incorporation or substitution) or removal (i.e., deletion or substitution) of the relevant amino acid residue(s). The nucleotide sequence may be conveniently modified by site-directed mutagenesis in accordance with conventional methods. Alternatively, the nucleotide sequence may be prepared by chemical synthesis, including but not limited to, by using an oligonucleotide synthesizer, wherein oligonucleotides are designed based on the amino acid sequence of the desired polypeptide, and preferably selecting those codons that are favored in the host cell in which the recombinant polypeptide will be produced. For example, several small oligonucleotides coding for portions of the desired polypeptide may be synthesized and assembled by PCR, ligation or ligation chain reaction. See, e.g., Barany, et al., *Proc. Natl. Acad. Sci.* 88: 189-193 (1991); U.S. Pat. No. 6,521,427 which are incorporated by reference herein.

This invention utilizes routine techniques in the field of recombinant genetics. Basic texts disclosing the general methods of use in this invention include Sambrook et al., *Molecular Cloning, A Laboratory Manual* (3rd ed. 2001); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel et al., eds., 1994).

General texts which describe molecular biological techniques include Berger and Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152* Academic Press, Inc., San Diego, Calif. (Berger); Sambrook et al., *Molecular Cloning—A Laboratory Manual (2nd Ed.)*, Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989 ("Sambrook") and *Current Protocols in Molecular Biology*, F. M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 1999) ("Ausubel"). These texts describe mutagenesis, the use of vectors, promoters and many other relevant topics related to, including but not limited to, the generation of genes or polynucleotides that include selector codons for production of proteins that include unnatural amino acids, orthogonal tRNAs, orthogonal synthetases, and pairs thereof.

Various types of mutagenesis are used in the invention for a variety of purposes, including but not limited to, to produce novel synthetases or tRNAs, to mutate tRNA molecules, to mutate polynucleotides encoding synthetases, to produce libraries of tRNAs, to produce libraries of synthetases, to produce selector codons, to insert selector codons that encode unnatural amino acids in a protein or polypeptide of interest. They include but are not limited to site-directed, random point

mutagenesis, homologous recombination, DNA shuffling or other recursive mutagenesis methods, chimeric construction, mutagenesis using uracil containing templates, oligonucleotide-directed mutagenesis, phosphorothioate-modified DNA mutagenesis, mutagenesis using gapped duplex DNA or the like, or any combination thereof. Additional suitable methods include point mismatch repair, mutagenesis using repair-deficient host strains, restriction-selection and restriction-purification, deletion mutagenesis, mutagenesis by total gene synthesis, double-strand break repair, and the like. Mutagenesis, including but not limited to, involving chimeric constructs, are also included in the present invention. In one embodiment, mutagenesis can be guided by known information of the naturally occurring molecule or altered or mutated naturally occurring molecule, including but not limited to, sequence, sequence comparisons, physical properties, secondary, tertiary, or quaternary structure, crystal structure or the like.

The texts and examples found herein describe these procedures. Additional information is found in the following publications and references cited within: Ling et al., *Approaches to DNA mutagenesis: an overview*, *Anal Biochem.* 254(2): 157-178 (1997); Dale et al., *Oligonucleotide-directed random mutagenesis using the phosphorothioate method*, *Methods Mol. Biol.* 57:369-374 (1996); Smith, *In vitro mutagenesis*, *Ann. Rev. Genet.* 19:423-462 (1985); Botstein & Shortie, *Strategies and applications of in vitro mutagenesis*, *Science* 229:1193-1201 (1985); Carter, *Site-directed mutagenesis*, *Biochem. J.* 237:1-7 (1986); Kunkel, *The efficiency of oligonucleotide directed mutagenesis*, in *Nucleic Acids & Molecular Biology* (Eckstein, F. and Lilley, D. M. J. eds., Springer Verlag, Berlin) (1987); Kunkel, *Rapid and efficient site-specific mutagenesis without phenotypic selection*, *Proc. Natl. Acad. Sci. USA* 82:488-492 (1985); Kunkel et al., *Rapid and efficient site-specific mutagenesis without phenotypic selection*, *Methods in Enzymol.* 154, 367-382 (1987); Bass et al., *Mutant Trp repressors with new DNA-binding specificities*, *Science* 242:240-245 (1988); Zoller & Smith, *Oligonucleotide-directed mutagenesis using M13-derived vectors: an efficient and general procedure for the production of point mutations in any DNA fragment*, *Nucleic Acids Res.* 10:6487-6500 (1982); Zoller & Smith, *Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors*, *Methods in Enzymol.* 100:468-500 (1983); Zoller & Smith, *Oligonucleotide-directed mutagenesis: a simple method using two oligonucleotide primers and a single-stranded DNA template*, *Methods in Enzymol.* 154:329-350 (1987); Taylor et al., *The use of phosphorothioate-modified DNA in restriction enzyme reactions to prepare nicked DNA*, *Nucl. Acids Res.* 13: 8749-8764 (1985); Taylor et al., *The rapid generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA*, *Nucl. Acids Res.* 13: 8765-8785 (1985); Nakamaye & Eckstein, *Inhibition of restriction endonuclease Nci I cleavage by phosphorothioate groups and its application to oligonucleotide-directed mutagenesis*, *Nucl. Acids Res.* 14: 9679-9698 (1986); Sayers et al., *5'-3' Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis*, *Nucl. Acids Res.* 16:791-802 (1988); Sayers et al., *Strand specific cleavage of phosphorothioate-containing DNA by reaction with restriction endonucleases in the presence of ethidium bromide*, (1988) *Nucl. Acids Res.* 16: 803-814; Kramer et al., *The gapped duplex DNA approach to oligonucleotide-directed mutation construction*, *Nucl. Acids Res.* 12: 9441-9456 (1984); Kramer & Fritz *Oligonucleotide-directed construction of mutations via gapped duplex DNA*, *Methods in Enzymol.* 154:350-367 (1987); Kramer et al., *Improved enzymatic in*

vitro reactions in the gapped duplex DNA approach to oligonucleotide-directed construction of mutations, *Nucl. Acids Res.* 16: 7207 (1988); Fritz et al., *Oligonucleotide-directed construction of mutations: a gapped duplex DNA procedure without enzymatic reactions in vitro*, *Nucl. Acids Res.* 16: 6987-6999 (1988); Kramer et al., *Different base/base mismatches are corrected with different efficiencies by the methyl-directed DNA mismatch-repair system of E. coli*, *Cell* 38:879-887 (1984); Carter et al., *Improved oligonucleotide site-directed mutagenesis using M13 vectors*, *Nucl. Acids Res.* 13: 4431-4443 (1985); Carter, *Improved oligonucleotide-directed mutagenesis using M13 vectors*, *Methods in Enzymol.* 154: 382-403 (1987); Eghtedarzadeh & Henikoff, *Use of oligonucleotides to generate large deletions*, *Nucl. Acids Res.* 14: 5115 (1986); Wells et al., *Importance of hydrogen-bond formation in stabilizing the transition state of subtilisin*, *Phil. Trans. R. Soc. Lond. A* 317: 415-423 (1986); Nambiar et al., *Total synthesis and cloning of a gene coding for the ribonuclease S protein*, *Science* 223: 1299-1301 (1984); Sakmar and Khorana, *Total synthesis and expression of a gene for the alpha-subunit of bovine rod outer segment guanine nucleotide-binding protein (transducin)*, *Nucl. Acids Res.* 14: 6361-6372 (1988); Wells et al., *Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites*, *Gene* 34:315-323 (1985); Grundström et al., *Oligonucleotide-directed mutagenesis by microscale 'shot-gun' gene synthesis*, *Nucl. Acids Res.* 13: 3305-3316 (1985); Mandecki, *Oligonucleotide-directed double-strand break repair in plasmids of Escherichia coli: a method for site-specific mutagenesis*, *Proc. Natl. Acad. Sci. USA*, 83:7177-7181 (1986); Arnold, *Protein engineering for unusual environments*, *Current Opinion in Biotechnology* 4:450-455 (1993); Sieber, et al., *Nature Biotechnology*, 19:456-460 (2001); W. P. C. Stemmer, *Nature* 370, 389-91 (1994); and, I. A. Lorimer, I. Pastan, *Nucleic Acids Res.* 23, 3067-8 (1995). Additional details on many of the above methods can be found in *Methods in Enzymology* Volume 154, which also describes useful controls for trouble-shooting problems with various mutagenesis methods.

Oligonucleotides, e.g., for use in mutagenesis of the present invention, e.g., mutating libraries of synthetases, or altering tRNAs, are typically synthesized chemically according to the solid phase phosphoramidite triester method described by Beaucage and Caruthers, *Tetrahedron Letts.* 22(20):1859-1862, (1981) e.g., using an automated synthesizer, as described in Needham-VanDevanter et al., *Nucleic Acids Res.*, 12:6159-6168 (1984).

The invention also relates to eukaryotic host cells, non-eukaryotic host cells, and organisms for the in vivo incorporation of an unnatural amino acid via orthogonal tRNA/RS pairs. Host cells are genetically engineered (including but not limited to, transformed, transduced or transfected) with the polynucleotides of the invention or constructs which include a polynucleotide of the invention, including but not limited to, a vector of the invention, which can be, for example, a cloning vector or an expression vector. For example, the coding regions for the orthogonal tRNA, the orthogonal tRNA synthetase, and the protein to be derivatized are operably linked to gene expression control elements that are functional in the desired host cell. The vector can be, for example, in the form of a plasmid, a cosmid, a phage, a bacterium, a virus, a naked polynucleotide, or a conjugated polynucleotide. The vectors are introduced into cells and/or microorganisms by standard methods including electroporation (Fromm et al., *Proc. Natl. Acad. Sci. USA* 82, 5824 (1985)), infection by viral vectors, high velocity ballistic penetration by small particles with the

nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., *Nature* 327, 70-73 (1987)), and/or the like.

The engineered host cells can be cultured in conventional nutrient media modified as appropriate for such activities as, for example, screening steps, activating promoters or selecting transformants. These cells can optionally be cultured into transgenic organisms. Other useful references, including but not limited to for cell isolation and culture (e.g., for subsequent nucleic acid isolation) include Freshney (1994) *Culture of Animal Cells, a Manual of Basic Technique*, third edition, Wiley-Liss, New York and the references cited therein; Payne et al., (1992) *Plant Cell and Tissue Culture in Liquid Systems* John Wiley & Sons, Inc. New York, N.Y.; Gamborg and Phillips (eds.) (1995) *Plant Cell, Tissue and Organ Culture*; Fundamental Methods Springer Lab Manual, Springer-Verlag (Berlin Heidelberg New York) and Atlas and Parks (eds.) *The Handbook of Microbiological Media* (1993) CRC Press, Boca Raton, Fla.

Several well-known methods of introducing target nucleic acids into cells are available, any of which can be used in the invention. These include: fusion of the recipient cells with bacterial protoplasts containing the DNA, electroporation, projectile bombardment, and infection with viral vectors (discussed further, below), etc. Bacterial cells can be used to amplify the number of plasmids containing DNA constructs of this invention. The bacteria are grown to log phase and the plasmids within the bacteria can be isolated by a variety of methods known in the art (see, for instance, Sambrook). In addition, kits are commercially available for the purification of plasmids from bacteria, (see, e.g., EasyPrep™, FlexiPrep™, both from Pharmacia Biotech; StrataClean™ from Stratagene; and, QIAprep™ from Qiagen). The isolated and purified plasmids are then further manipulated to produce other plasmids, used to transfect cells or incorporated into related vectors to infect organisms. Typical vectors contain transcription and translation terminators, transcription and translation initiation sequences, and promoters useful for regulation of the expression of the particular target nucleic acid. The vectors optionally comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the cassette in eukaryotes, or prokaryotes, or both, (including but not limited to, shuttle vectors) and selection markers for both prokaryotic and eukaryotic systems. Vectors are suitable for replication and integration in prokaryotes, eukaryotes, or both. See, Gillam & Smith, *Gene* 8:81 (1979); Roberts, et al., *Nature*, 328:731 (1987); Schneider, E., et al., *Protein Expr. Purif.* 6(1):10-14 (1995); Ausubel, Sambrook, Berger (all supra). A catalogue of bacteria and bacteriophages useful for cloning is provided, e.g., by the ATCC, e.g., *The ATCC Catalogue of Bacteria and Bacteriophage* (1992) Gherna et al. (eds) published by the ATCC. Additional basic procedures for sequencing, cloning and other aspects of molecular biology and underlying theoretical considerations are also found in Watson et al. (1992) *Recombinant DNA Second Edition* Scientific American Books, NY. In addition, essentially any nucleic acid (and virtually any labeled nucleic acid, whether standard or non-standard) can be custom or standard ordered from any of a variety of commercial sources, such as the Midland Certified Reagent Company (Midland, Tex. available on the World Wide Web at mcr.com), The Great American Gene Company (Ramona, Calif. available on the World Wide Web at genco.com), ExpressGen Inc. (Chicago, Ill. available on the World Wide Web at expressgen.com), Operon Technologies Inc. (Alameda, Calif.) and many others.

Selector Codons

Selector codons of the invention expand the genetic codon framework of protein biosynthetic machinery. For example, a selector codon includes, but is not limited to, a unique three base codon, a nonsense codon, such as a stop codon, including but not limited to, an amber codon (UAG), an ochre codon, or an opal codon (UGA), an unnatural codon, a four or more base codon, a rare codon, or the like. It is readily apparent to those of ordinary skill in the art that there is a wide range in the number of selector codons that can be introduced into a desired gene or polynucleotide, including but not limited to, one or more, two or more, three or more, 4, 5, 6, 7, 8, 9, 10 or more in a single polynucleotide encoding at least a portion of the hPP polypeptide.

In one embodiment, the methods involve the use of a selector codon that is a stop codon for the incorporation of one or more unnatural amino acids in vivo. For example, an O-tRNA is produced that recognizes the stop codon, including but not limited to, UAG, and is aminoacylated by an O-RS with a desired unnatural amino acid. This O-tRNA is not recognized by the naturally occurring host's aminoacyl-tRNA synthetases. Conventional site-directed mutagenesis can be used to introduce the stop codon, including but not limited to, TAG, at the site of interest in a polypeptide of interest. See, e.g., Sayers, J. R., et al. (1988), *5'-3' Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis. Nucleic Acids Res* 16:791-802. When the O-RS, O-tRNA and the nucleic acid that encodes the polypeptide of interest are combined in vivo, the unnatural amino acid is incorporated in response to the HAG codon to give a polypeptide containing the unnatural amino acid at the specified position.

The incorporation of unnatural amino acids in vivo can be done without significant perturbation of the eukaryotic host cell. For example, because the suppression efficiency for the UAG codon depends upon the competition between the O-tRNA, including but not limited to, the amber suppressor tRNA, and a eukaryotic release factor (including but not limited to, eRF) (which binds to a stop codon and initiates release of the growing peptide from the ribosome), the suppression efficiency can be modulated by, including but not limited to, increasing the expression level of O-tRNA, and/or the suppressor tRNA.

Unnatural amino acids can also be encoded with rare codons. For example, when the arginine concentration in an in vitro protein synthesis reaction is reduced, the rare arginine codon, AGG, has proven to be efficient for insertion of Ala by a synthetic tRNA acylated with alanine. See, e.g., Ma et al., *Biochemistry*, 32:7939 (1993). In this case, the synthetic tRNA competes with the naturally occurring tRNA^{Arg}, which exists as a minor species in *Escherichia coli*. Some organisms do not use all triplet codons. An unassigned codon AGA in *Micrococcus luteus* has been utilized for insertion of amino acids in an in vitro transcription/translation extract. See, e.g., Kowal and Oliver, *Nucl. Acid. Res.*, 25:4685 (1997). Components of the present invention can be generated to use these rare codons in vivo.

Selector codons also comprise extended codons, including but not limited to, four or more base codons, such as, four, five, six or more base codons. Examples of four base codons include, but are not limited to, AGGA, CUAG, UAGA, CCCU and the like. Examples of five base codons include, but are not limited to, AGGAC, CCCC, CCCUC, CUAGA, CUACU, UAGGC and the like. A feature of the invention includes using extended codons based on frameshift suppression. Four or more base codons can insert, including but not limited to, one or multiple unnatural amino acids into the same protein. For example, in the presence of mutated O-tRNAs, including

but not limited to, a special frameshift suppressor tRNAs, with anticodon loops, for example, with at least 8-10 nt anticodon loops, the four or more base codon is read as single amino acid. In other embodiments, the anticodon loops can decode, including but not limited to, at least a four-base codon, at least a five-base codon, or at least a six-base codon or more. Since there are 256 possible four-base codons, multiple unnatural amino acids can be encoded in the same cell using a four or more base codon. See, Anderson et al., (2002) *Exploring the Limits of Codon and Anticodon Size, Chemistry and Biology*, 9:237-244; Magliery, (2001) *Expanding the Genetic Code: Selection of Efficient Suppressors of Four-base Codons and Identification of "Shifty" Four-base Codons with a Library Approach in Escherichia coli*, *J. Mol. Biol.* 307: 755-769.

For example, four-base codons have been used to incorporate unnatural amino acids into proteins using in vitro biosynthetic methods. See, e.g., Ma et al., (1993) *Biochemistry*, 32:7939; and Hohsaka et al., (1999) *J. Am. Chem. Soc.*, 121: 34. CGGG and AGGU were used to simultaneously incorporate 2-naphthylalanine and an NBD derivative of lysine into streptavidin in vitro with two chemically acylated frameshift suppressor tRNAs. See, e.g., Hohsaka et al., (1999) *J. Am. Chem. Soc.*, 121:12194. In an in vivo study, Moore et al. examined the ability of tRNA^{Leu} derivatives with NCUA anticodons to suppress UAGN codons (N can be U, A, O, or C), and found that the quadruplet UAGA can be decoded by a tRNA^{Leu} with a UCUA anticodon with an efficiency of 13 to 26% with little decoding in the 0 or -1 frame. See, Moore et al., (2000) *J. Mol. Biol.*, 298:195. In one embodiment, extended codons based on rare codons or nonsense codons can be used in the present invention, which can reduce mis-sense readthrough and frameshift suppression at other unwanted sites.

For a given system, a selector codon can also include one of the natural three base codons, where the endogenous system does not use (or rarely uses) the natural base codon. For example, this includes a system that is lacking a tRNA that recognizes the natural three base codon, and/or a system where the three base codon is a rare codon.

Selector codons optionally include unnatural base pairs. These unnatural base pairs further expand the existing genetic alphabet. One extra base pair increases the number of triplet codons from 64 to 125. Properties of third base pairs include stable and selective base pairing, efficient enzymatic incorporation into DNA with high fidelity by a polymerase, and the efficient continued primer extension after synthesis of the nascent unnatural base pair. Descriptions of unnatural base pairs which can be adapted for methods and compositions include, e.g., Hirao, et al., (2002) *An unnatural base pair for incorporating amino acid analogues into protein*, *Nature Biotechnology*, 20:177-182. See, also, Wu, Y., et al., (2002) *J. Am. Chem. Soc.* 124:14626-14630. Other relevant publications are listed below.

For in vivo usage, the unnatural nucleoside is membrane permeable and is phosphorylated to form the corresponding triphosphate. In addition, the increased genetic information is stable and not destroyed by cellular enzymes. Previous efforts by Benner and others took advantage of hydrogen bonding patterns that are different from those in canonical Watson-Crick pairs, the most noteworthy example of which is the iso-C:iso-G pair. See, e.g., Switzer et al., (1989) *J. Am. Chem. Soc.*, 111:8322; and Piccirilli et al., (1990) *Nature*, 343:33; Kool, (2000) *Curr. Opin. Chem. Biol.*, 4:602. These bases in general mispair to some degree with natural bases and cannot be enzymatically replicated. Kool and co-workers demonstrated that hydrophobic packing interactions between bases

can replace hydrogen bonding to drive the formation of base pair. See, Kool, (2000) *Curr. Opin. Chem. Biol.*, 4:602; and Guckian and Kool, (1998) *Angew. Chem. Int. Ed. Engl.*, 36, 2825. In an effort to develop an unnatural base pair satisfying all the above requirements, Schultz, Romesberg and co-workers have systematically synthesized and studied a series of unnatural hydrophobic bases. A PICS:PICS self-pair is found to be more stable than natural base pairs, and can be efficiently incorporated into DNA by Klenow fragment of *Escherichia coli* DNA polymerase I (KF). See, e.g., McMinn et al., (1999) *J. Am. Chem. Soc.*, 121:11585-6; and Ogawa et al., (2000) *J. Am. Chem. Soc.*, 122:3274. A 3MN:3MN self-pair can be synthesized by KF with efficiency and selectivity sufficient for biological function. See, e.g., Ogawa et al., (2000) *J. Am. Chem. Soc.*, 122:8803. However, both bases act as a chain terminator for further replication. A mutant DNA polymerase has been recently evolved that can be used to replicate the PICS self pair. In addition, a 7AI self pair can be replicated. See, e.g., Tae et al., (2001) *J. Am. Chem. Soc.*, 123:7439. A novel metallobase pair, Dipic:Py, has also been developed, which forms a stable pair upon binding Cu(II). See, Meggers et al., (2000) *J. Am. Chem. Soc.*, 122:10714. Because extended codons and unnatural codons are intrinsically orthogonal to natural codons, the methods of the invention can take advantage of this property to generate orthogonal tRNAs for them.

A translational bypassing system can also be used to incorporate an unnatural amino acid in a desired polypeptide. In a translational bypassing system, a large sequence is incorporated into a gene but is not translated into protein. The sequence contains a structure that serves as a cue to induce the ribosome to hop over the sequence and resume translation downstream of the insertion.

In certain embodiments, the protein or polypeptide of interest (or portion thereof) in the methods and/or compositions of the invention is encoded by a nucleic acid. Typically, the nucleic acid comprises at least one selector codon, at least two selector codons, at least three selector codons, at least four selector codons, at least five selector codons, at least six selector codons, at least seven selector codons, at least eight selector codons, at least nine selector codons, ten or more selector codons.

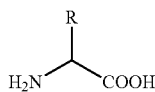
Genes coding for proteins or polypeptides of interest can be mutagenized using methods known to one of ordinary skill in the art and described herein to include, for example, one or more selector codon for the incorporation of an unnatural amino acid. For example, a nucleic acid for a protein of interest is mutagenized to include one or more selector codon, providing for the incorporation of one or more unnatural amino acids. The invention includes any such variant, including but not limited to, mutant, versions of any protein, for example, including at least one unnatural amino acid. Similarly, the invention also includes corresponding nucleic acids, i.e., any nucleic acid with one or more selector codon that encodes one or more unnatural amino acid.

Nucleic acid molecules encoding a protein of interest such as an hPP polypeptide may be readily mutated to introduce a cysteine at any desired position of the polypeptide. Cysteine is widely used to introduce reactive molecules, water soluble polymers, proteins, or a wide variety of other molecules, onto a protein of interest. Methods suitable for the incorporation of cysteine into a desired position of a polypeptide are known to those of ordinary skill in the art, such as those described in U.S. Pat. No. 6,608,183, which is incorporated by reference herein, and standard mutagenesis techniques.

IV. Non-naturally Encoded Amino Acids

A very wide variety of non-naturally encoded amino acids are suitable for use in the present invention. Any number of non-naturally encoded amino acids can be introduced into an hPP polypeptide. In general, the introduced non-naturally encoded amino acids are substantially chemically inert toward the 20 common, genetically-encoded amino acids (i.e., alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine). In some embodiments, the non-naturally encoded amino acids include side chain functional groups that react efficiently and selectively with functional groups not found in the 20 common amino acids (including but not limited to, azido, ketone, aldehyde and aminooxy groups) to form stable conjugates. For example, an hPP polypeptide that includes a non-naturally encoded amino acid containing an azido functional group can be reacted with a polymer (including but not limited to, poly (ethylene glycol) or, alternatively, a second polypeptide containing an alkyne moiety to form a stable conjugate resulting for the selective reaction of the azide and the alkyne functional groups to form a Huisgen [3+2] cycloaddition product.

The generic structure of an alpha-amino acid is illustrated as follows (Formula I):

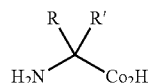
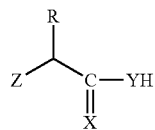


A non-naturally encoded amino acid is typically any structure having the above-listed formula wherein the R group is any substituent other than one used in the twenty natural amino acids, and may be suitable for use in the present invention. Because the non-naturally encoded amino acids of the invention typically differ from the natural amino acids only in the structure of the side chain, the non-naturally encoded amino acids form amide bonds with other amino acids, including but not limited to, natural or non-naturally encoded, in the same manner in which they are formed in naturally occurring polypeptides. However, the non-naturally encoded amino acids have side chain groups that distinguish them from the natural amino acids. For example, R optionally comprises an alkyl-, aryl-, acyl-, keto-, azido-, hydroxyl-, hydrazine, cyano-, halo-, hydrazide, alkenyl, alkynyl, ether, thiol, seleno-, sulfonyl-, borate, boronate, phospho, phosphono, phosphine, heterocyclic, enone, imine, aldehyde, ester, thioacid, hydroxylamine, amino group, or the like or any combination thereof. Other non-naturally occurring amino acids of interest that may be suitable for use in the present invention include, but are not limited to, amino acids comprising a photoactivatable cross-linker, spin-labeled amino acids, fluorescent amino acids, metal binding amino acids, metal-containing amino acids, radioactive amino acids, amino acids with novel functional groups, amino acids that covalently or noncovalently interact with other molecules, photocaged and/or photoisomerizable amino acids, amino acids comprising biotin or a biotin analogue, glycosylated amino acids such as a sugar substituted serine, other carbohydrate modified amino acids, keto-containing amino acids, amino acids comprising polyethylene glycol or polyether, heavy atom substituted amino acids, chemically cleavable and/or photocleavable amino acids, amino acids with an elongated side chains as compared to natural amino acids, includ-

ing but not limited to, polyethers or long chain hydrocarbons, including but not limited to, greater than about 5 or greater than about 10 carbons, carbon-linked sugar-containing amino acids, redox-active amino acids, amino thioacid containing amino acids, and amino acids comprising one or more toxic moiety.

Exemplary non-naturally encoded amino acids that may be suitable for use in the present invention and that are useful for reactions with water soluble polymers include, but are not limited to, those with carbonyl, aminooxy, hydrazine, hydrazide, semicarbazide, azide and alkyne reactive groups. In some embodiments, non-naturally encoded amino acids comprise a saccharide moiety. Examples of such amino acids include N-acetyl-L-glucosaminyl-L-serine, N-acetyl-L-galactosaminyl-L-serine, N-acetyl-L-glucosaminyl-L-threonine, N-acetyl-L-glucosaminyl-L-asparagine and O-mannosaminyl-L-serine. Examples of such amino acids also include examples where the naturally-occurring N- or O-linkage between the amino acid and the saccharide is replaced by a covalent linkage not commonly found in nature—including but not limited to, an alkene, an oxime, a thioether, an amide and the like. Examples of such amino acids also include saccharides that are not commonly found in naturally-occurring proteins such as 2-deoxy-glucose, 2-deoxygalactose and the like.

Many of the non-naturally encoded amino acids provided herein are commercially available, e.g., from Sigma-Aldrich (St. Louis, Mo., USA), Novabiochem (a division of EMD Biosciences, Darmstadt, Germany), or Peptech (Burlington, Mass., USA). Those that are not commercially available are optionally synthesized as provided herein or using standard methods known to those of ordinary skill in the art. For organic synthesis techniques, see, e.g., *Organic Chemistry* by Fessenden and Fessenden, (1982, Second Edition, Willard Grant Press, Boston Mass.); *Advanced Organic Chemistry* by March (Third Edition, 1985, Wiley and Sons, New York); and *Advanced Organic Chemistry* by Carey and Sundberg (Third Edition, Parts A and B, 1990, Plenum Press, New York). See, also, U.S. Patent Application Publications 2003/0082575 and 2003/0108885, which are incorporated by reference herein. In addition to unnatural amino acids that contain novel side chains, unnatural amino acids that may be suitable for use in the present invention also optionally comprise modified backbone structures, including but not limited to, as illustrated by the structures of Formula II and III:



wherein Z typically comprises OH, NH₂, SH, NH—R', or S—R'; X and Y, which can be the same or different, typically comprise S or O, and R and R', which are optionally the same or different, are typically selected from the same list of constituents for the R group described above for the unnatural amino acids having Formula I as well as hydrogen. For example, unnatural amino acids of the invention optionally comprise substitutions in the amino or carboxyl group as illustrated by Formulas II and III. Unnatural amino acids of

this type include, but are not limited to, α -hydroxy acids, α -thioacids, α -aminothiocarboxylates, including but not limited to, with side chains corresponding to the common twenty natural amino acids or unnatural side chains. In addition, substitutions at the α -carbon optionally include, but are not limited to, L, D, or α - α -disubstituted amino acids such as D-glutamate, D-alanine, D-methyl-O-tyrosine, aminobutyric acid, and the like. Other structural alternatives include cyclic amino acids, such as proline analogues as well as 3, 4, 6, 7, 8, and 9 membered ring proline analogues, β and γ amino acids such as substituted β -alanine and γ -amino butyric acid.

Many unnatural amino acids are based on natural amino acids, such as tyrosine, glutamine, phenylalanine, and the like, and are suitable for use in the present invention. Tyrosine analogs include, but are not limited to, para-substituted tyrosines, ortho-substituted tyrosines, and meta substituted tyrosines, where the substituted tyrosine comprises, including but not limited to, a keto group (including but not limited to, an acetyl group), a benzoyl group, an amino group, a hydrazine, an hydroxylamine, a thiol group, a carboxy group, an isopropyl group, a methyl group, a C_6 - C_{20} straight chain or branched hydrocarbon, a saturated or unsaturated hydrocarbon, an O-methyl group, a polyether group, a nitro group, an alkynyl group or the like. In addition, multiply substituted aryl rings are also contemplated. Glutamine analogs that may be suitable for use in the present invention include, but are not limited to, α -hydroxy derivatives, γ -substituted derivatives, cyclic derivatives, and amide substituted glutamine derivatives. Example phenylalanine analogs that may be suitable for use in the present invention include, but are not limited to, para-substituted phenylalanines, ortho-substituted phenylalanines, and meta-substituted phenylalanines, where the substituent comprises, including but not limited to, a hydroxy group, a methoxy group, a methyl group, an allyl group, an aldehyde, an azido, an iodo, a bromo, a keto group (including but not limited to, an acetyl group), a benzoyl, an alkynyl group, or the like. Specific examples of unnatural amino acids that may be suitable for use in the present invention include, but are not limited to, a p-acetyl-L-phenylalanine, an O-methyl-L-tyrosine, an L-3-(2-naphthyl)alanine, a 3-methyl-phenylalanine, an O-4-allyl-L-tyrosine, a 4-propyl-L-tyrosine, a tri-O-acetyl-GlnAc β -serine, an L-Dopa, a fluorinated phenylalanine, an isopropyl-L-phenylalanine, a p-azido-L-phenylalanine, a p-acyl-L-phenylalanine, a p-benzoyl-L-phenylalanine, an L-phosphoserine, a phosphoserine, a phosphotyrosine, a p-iodo-phenylalanine, a p-bromophenylalanine, a p-amino-L-phenylalanine, an isopropyl-L-phenylalanine, and a p-propargyloxy-phenylalanine, and the like. Examples of structures of a variety of unnatural amino acids that may be suitable for use in the present invention are provided in, for example, WO 2002/085923 entitled "In vivo incorporation of unnatural amino acids." See also Kiick et al., (2002) *Incorporation of azides into recombinant proteins for chemoselective modification by the Staudinger ligation*, PNAS 99:19-24, which is incorporated by reference herein, for additional methionine analogs.

In one embodiment, compositions of an hPP polypeptide that include an unnatural amino acid (such as p-(propargyloxy)-phenylalanine) are provided. Various compositions comprising p-(propargyloxy)-phenylalanine and, including but not limited to, proteins and/or cells, are also provided. In one aspect, a composition that includes the p-(propargyloxy)-phenylalanine unnatural amino acid, further includes an orthogonal tRNA. The unnatural amino acid can be bonded (including but not limited to, covalently) to the orthogonal tRNA, including but not limited to, covalently bonded to the

orthogonal tRNA though an amino-acyl bond, covalently bonded to a 3'OH or a 2'OH of a terminal ribose sugar of the orthogonal tRNA, etc.

The chemical moieties via unnatural amino acids that can be incorporated into proteins offer a variety of advantages and manipulations of the protein. For example, the unique reactivity of a keto functional group allows selective modification of proteins with any of a number of hydrazine- or hydroxylamine-containing reagents in vitro and in vivo. A heavy atom unnatural amino acid, for example, can be useful for phasing X-ray structure data. The site-specific introduction of heavy atoms using unnatural amino acids also provides selectivity and flexibility in choosing positions for heavy atoms. Photo-reactive unnatural amino acids (including but not limited to, amino acids with benzophenone and arylazides (including but not limited to, phenylazide) side chains), for example, allow for efficient in vivo and in vitro photo crosslinking of protein. Examples of photoreactive unnatural amino acids include, but are not limited to, p-azido-phenylalanine and p-benzoyl-phenylalanine. The protein with the photoreactive unnatural amino acids can then be crosslinked at will by excitation of the photoreactive group-providing temporal control. In one example, the methyl group of an unnatural amino can be substituted with an isotopically labeled, including but not limited to, methyl group, as a probe of local structure and dynamics, including but not limited to, with the use of nuclear magnetic resonance and vibrational spectroscopy. Alkynyl or azido functional groups, for example, allow the selective modification of proteins with molecules through a [3+2] cycloaddition reaction.

A non-natural amino acid incorporated into a polypeptide at the amino terminus can be composed of an R group that is any substituent other than one used in the twenty natural amino acids and a 2nd reactive group different from the NH₂ group normally present in α -amino acids (see Formula I). A similar non-natural amino acid can be incorporated at the carboxyl terminus with a 2nd reactive group different from the COOH group normally present in α -amino acids (see Formula I).

The unnatural amino acids of the invention may be selected or designed to provide additional characteristics unavailable in the twenty natural amino acids. For example, unnatural amino acid may be optionally designed or selected to modify the biological properties of a protein, e.g., into which they are incorporated. For example, the following properties may be optionally modified by inclusion of an unnatural amino acid into a protein: toxicity, biodistribution, solubility, stability, e.g., thermal, hydrolytic, oxidative, resistance to enzymatic degradation, and the like, facility of purification and processing, structural properties, spectroscopic properties, chemical and/or photochemical properties, catalytic activity, redox potential, half-life, ability to react with other molecules, e.g., covalently or noncovalently, and the like.

Structure and Synthesis of Non-natural Amino Acids: Carbonyl, Carbonyl-like, Masked Carbonyl, Protected Carbonyl Groups, and Hydroxylamine Groups

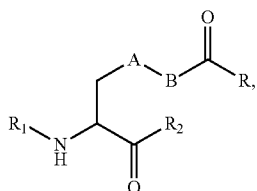
In some embodiments the present invention provides hPP or hA or hFc linked to a water soluble polymer, e.g., a PEG, by an oxime bond.

Many types of non-naturally encoded amino acids are suitable for formation of oxime bonds. These include, but are not limited to, non-naturally encoded amino acids containing a carbonyl, dicarbonyl, or hydroxylamine group. Such amino acids are described in U.S. Patent Publication Nos. 2006/0194256, 2006/0217532, and 2006/0217289 and WO 2006/069246 entitled "Compositions containing, methods involving, and uses of non-natural amino acids and polypeptides,"

with a proviso that when A is phenylene and each R₃ is H, B is present; and that when A is —(CH₂)₄— and each R₃ is H, B is not —NHC(O)(CH₂CH₂)—; and that when A and B are absent and each R₃ is H, R is not methyl.

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In addition, having the structure of Formula (V) are included:



wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkenylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

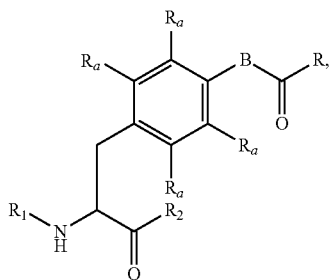
B is optional, and when present is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-, —S(O)_k— where k is 1, 2, or 3, —S(O)_k(alkylene or substituted alkylene)-, —C(O)—, —C(O)-(alkylene or substituted alkylene)-, —C(S)—, —C(S)-(alkylene or substituted alkylene)-, —N(R')—, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')—, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')—, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O—, —S(O)_kN(R')—, —N(R')C(O)N(R')—, —N(R')C(S)N(R')—, —N(R')S(O)_kN(R')—, —N(R')—N=, —C(R')—N=, —C(R')=N—N(R')—, —C(R')=N—N=, —C(R')₂—N=N—, and —C(R')₂—N(R')—N(R')—, where each R' is independently H, alkyl, or substituted alkyl;

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide; with a proviso that when A is phenylene, B is present; and that when A is —(CH₂)₄—, B is not —NHC(O)(CH₂CH₂)—; and that when A and B are absent, R is not methyl.

In addition, amino acids having the structure of Formula (VI) are included:



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wherein:

B is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-, —S(O)_k— where k is 1, 2, or 3, —S(O)_k(alkylene or substituted alkylene)-, —C(O)—, —C(O)-(alkylene or substituted alkylene)-, —C(S)—, —C(S)-(alkylene or substituted alkylene)-, —N(R')—, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')—, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')—, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O—, —S(O)_kN(R')—, —N(R')C(O)N(R')—, —N(R')C(S)N(R')—, —N(R')S(O)_kN(R')—, —N(R')—N=, —C(R')—N=, —C(R')=N—N(R')—, —C(R')=N—N=, —C(R')₂—N=N—, and —C(R')₂—N(R')—N(R')—, where each R' is independently H, alkyl, or substituted alkyl;

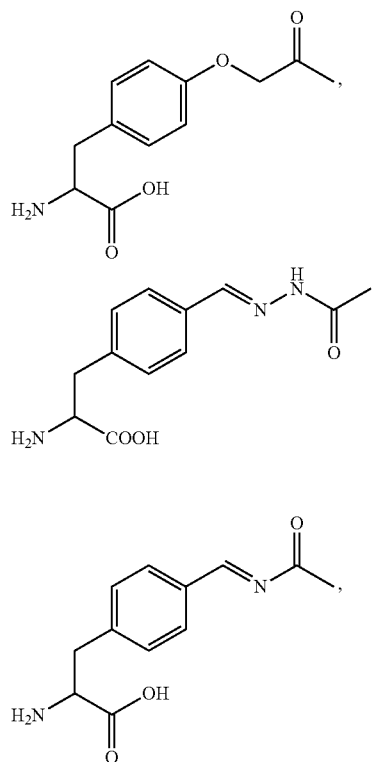
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

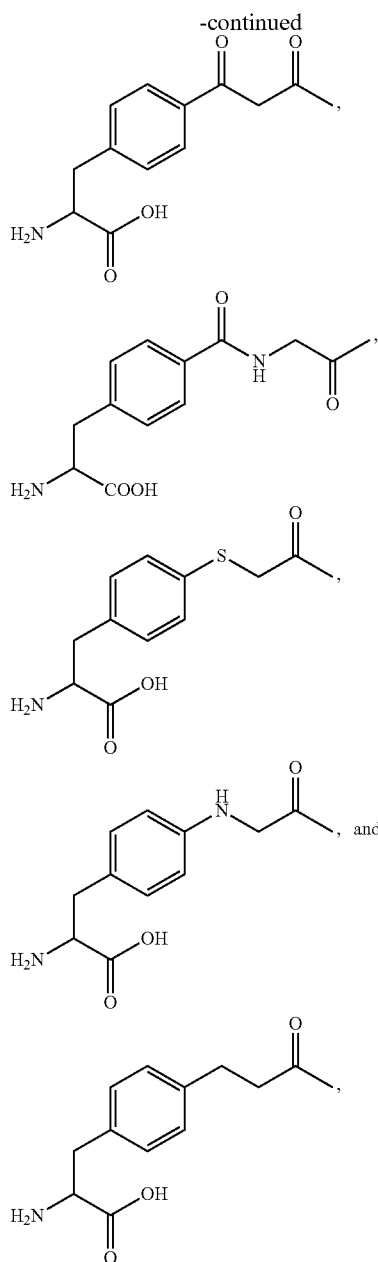
R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

each R_a is independently selected from the group consisting of H, halogen, alkyl, substituted alkyl, —N(R')₂, —C(O)R', where k is 1, 2, or 3, —C(O)N(R')₂, —OR', and —S(O)_kR', where each R' is independently H, alkyl, or substituted alkyl.

In addition, the following amino acids are included:

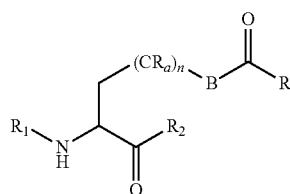


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wherein such compounds are optionally amino protected
group, carboxyl protected or a salt thereof. In addition, any of
the following non-natural amino acids may be incorporated
into a non-natural amino acid polypeptide.

In addition, the following amino acids having the structure
of Formula (VII) are included:



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wherein

B is optional, and when present is a linker selected from the
group consisting of lower alkylene, substituted lower alkyl-
ylene, lower alkenylene, substituted lower alkenylene,
lower heteroalkylene, substituted lower heteroalkylene,
—O—, —O-(alkylene or substituted alkylene)-, —S—,
—S-(alkylene or substituted alkylene)-, —S(O)_k— where
k is 1, 2, or 3, —S(O)_k(alkylene or substituted alkylene)-,
—C(O)—, —C(O)-(alkylene or substituted alkylene)-,
—C(S)—, —C(S)-(alkylene or substituted alkylene)-,
—NR'-(alkylene or substituted alkylene)-, —C(O)N
(R')—, —CON(R')-(alkylene or substituted alkylene)-,
—CSN(R')—, —CSN(R')-(alkylene or substituted alkyl-
ylene)-, —N(R')CO-(alkylene or substituted alkylene)-,
—N(R')C(O)O—, —S(O)_kN(R')—, —N(R')C(O)N
(R')—, —N(R')C(S)N(R')—, —N(R')S(O)_kN(R')—,
—N(R')—N=, —C(R')—N=, —C(R')=N—N(R')—,
—C(R')=N—N=, —C(R')₂—N=N—, and —C(R')₂—
N(R')—N(R')—, where each R' is independently H, alkyl,
or substituted alkyl;

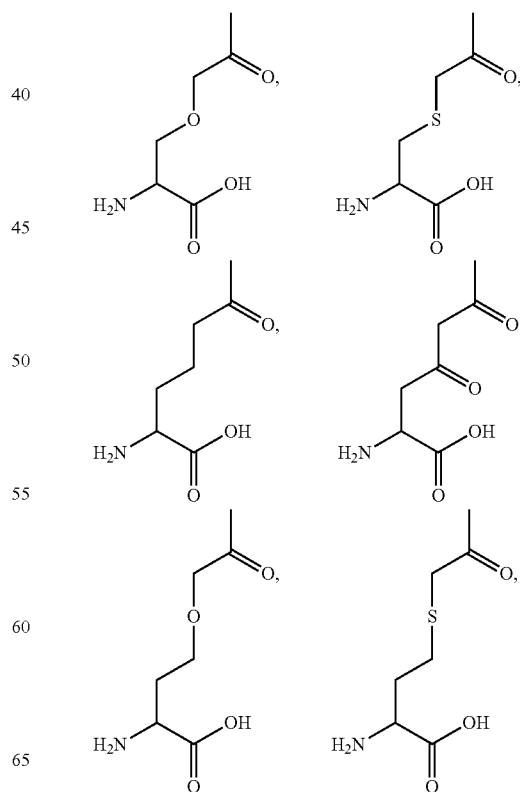
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted
cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting
group, resin, amino acid, polypeptide, or polynucleotide;
and

R₂ is optional, and when present, is OH, an ester protecting
group, resin, amino acid, polypeptide, or polynucleotide;
each R_a is independently selected from the group consisting
of H, halogen, alkyl, substituted alkyl, —N(R')₂,
—C(O)_kR' where k is 1, 2, or 3, —C(O)N(R')₂, —OR', and
—S(O)_kR', where each R' is independently H, alkyl, or
substituted alkyl; and n is 0 to 8;

with a proviso that when A is —(CH₂)₄—, B is not —NHC
(O)(CH₂CH₂)—.

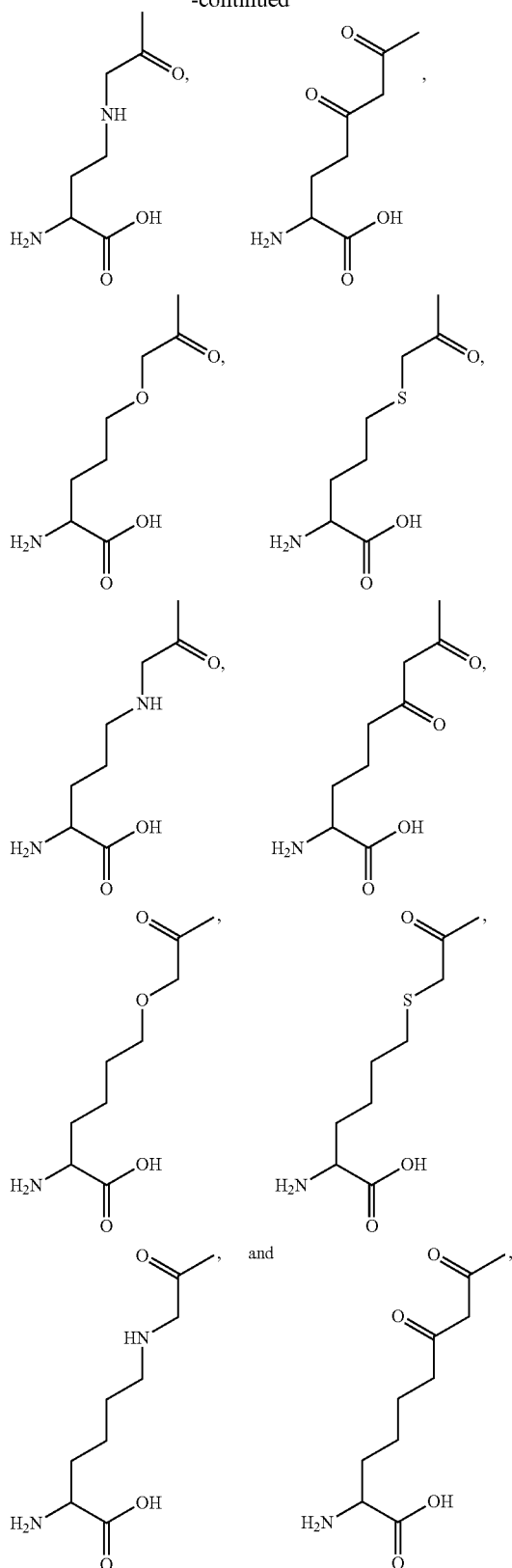
In addition, the following amino acids are included:



(VII)

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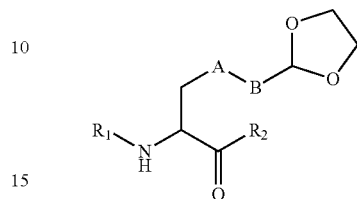


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non-natural amino acids and any of the following non-natural amino acids may be incorporated into a non-natural amino acid polypeptide.

In addition, the following amino acids having the structure of Formula (VIII) are included:

(VIII)



wherein A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

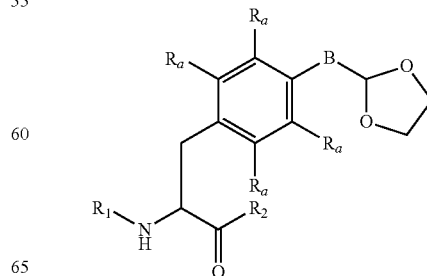
B is optional, and when present is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-, —S(O)_k— where k is 1, 2, or 3, —S(O)_k-(alkylene or substituted alkylene)-, —C(O)—, —C(O)-(alkylene or substituted alkylene)-, —C(S)—, —C(S)-(alkylene or substituted alkylene)-, —N(R')—, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')—, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')—, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O—, —S(O)_kN(R')—, —N(R')C(O)N(R')—, —N(R')C(S)N(R')—, —N(R')S(O)_kN(R')—, —N(R')—N=, —C(R')=N—, —C(R')=N—N(R')—, —C(R')=N—N=, —C(R')₂=N=N—, and —C(R')₂=N(R')—N(R')—, where each R' is independently H, alkyl, or substituted alkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide.

In addition, the following amino acids having the structure of Formula (IX) are included:

(IX)



wherein such compounds are optionally amino protected, optionally carboxyl protected, optionally amino protected and carboxyl protected, or a salt thereof. In addition, these

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B is optional, and when present is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-, —S(O)_k— where k is 1, 2, or 3, —S(O)_k-(alkylene or substituted alkylene)-, —C(O)—, —C(O)-(alkylene or substituted alkylene)-, —C(S)—, —C(S)-(alkylene or substituted alkylene)-, —N(R')—, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')—, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')—, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O—, —S(O)_kN(R')—, —N(R')C(O)N(R')—, —N(R')C(S)N(R')—, —N(R')S(O)_kN(R')—, —N(R')—N=, —C(R')=N—, —C(R')=N—N(R')—, —C(R')=N—N=, —C(R')₂—N=N—, and —C(R')₂—N(R')—N(R')—, where each R' is independently H, alkyl, or substituted alkyl;

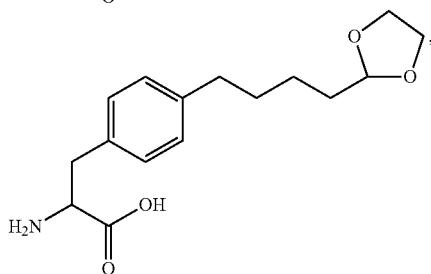
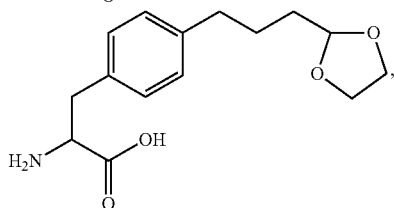
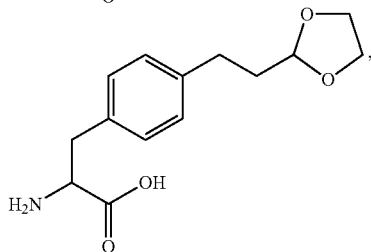
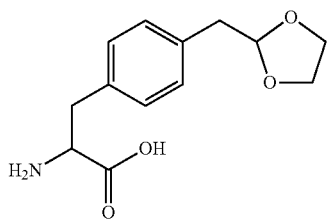
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

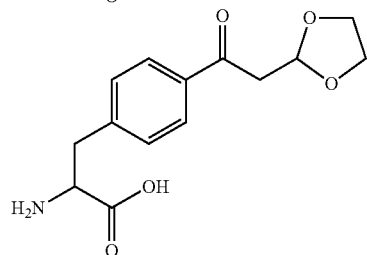
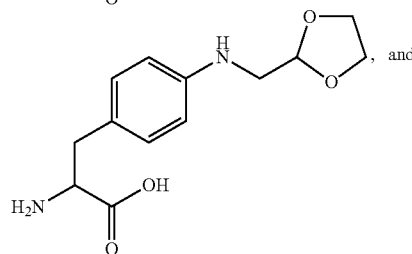
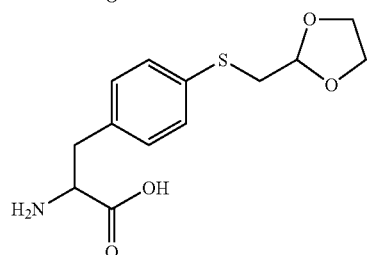
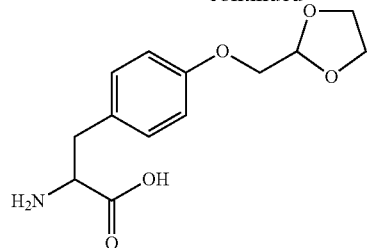
wherein each R_a is independently selected from the group consisting of H, halogen, alkyl, substituted alkyl, —N(R')₂, —C(O)_kR' where k is 1, 2, or 3, —C(O)N(R')₂, —OR', and —S(O)_kR', where each R' is independently H, alkyl, or substituted alkyl.

In addition, the following amino acids are included:



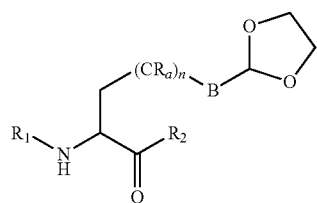
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wherein such compounds are optionally amino protected, optionally carboxyl protected, optionally amino protected and carboxyl protected, or a salt thereof. In addition, these non-natural amino acids and any of the following non-natural amino acids may be incorporated into a non-natural amino acid polypeptide.

In addition, the following amino acids having the structure of Formula (X) are included:



wherein B is optional, and when present is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-,

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—S(O)_k— where k is 1, 2, or 3, —S(O)_k(alkylene or substituted alkylene)-, —C(O)-, —C(O)-(alkylene or substituted alkylene)-, —C(S)-, —C(S)-(alkylene or substituted alkylene)-, —N(R')-, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')-, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')-, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O-, —S(O)_kN(R')-, —N(R')C(O)N(R')-, —N(R')C(S)N(R')-, —N(R')S(O)_kN(R')-, —N(R')—N=, —C(R')=N-, —C(R')=N—N(R')-, —C(R')=N—N=, —C(R')₂—N=N-, and —C(R')₂—N(R')—N(R')-, where each R' is independently H, alkyl, or substituted alkyl;

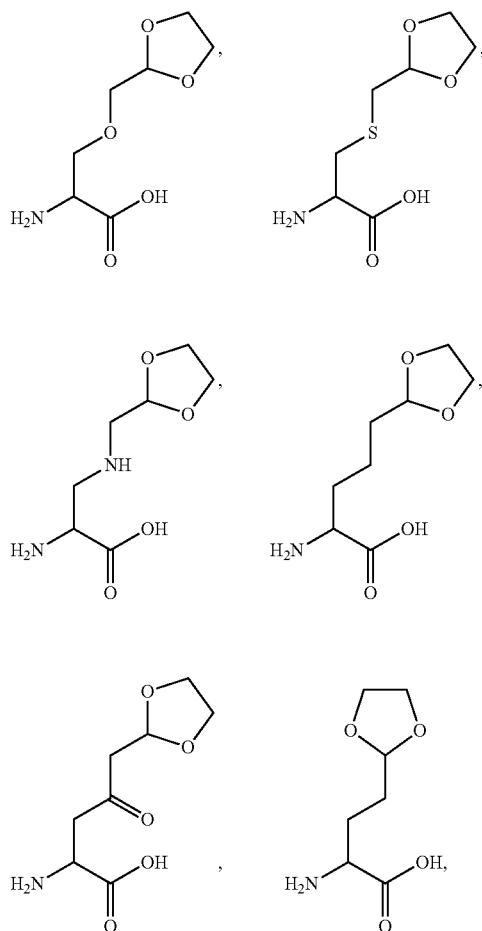
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

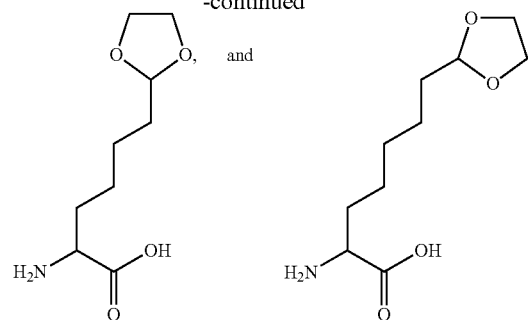
each R_a is independently selected from the group consisting of H, halogen, alkyl, substituted alkyl, —N(R')₂-, —C(O)_kR' where k is 1, 2, or 3, —C(O)N(R')₂-, —OR', and —S(O)_kR', where each R' is independently H, alkyl, or substituted alkyl; and n is 0 to 8.

In addition, the following amino acids are included:



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wherein such compounds are optionally amino protected, optionally carboxyl protected, optionally amino protected and carboxyl protected, or a salt thereof. In addition, these non-natural amino acids and any of the following non-natural amino acids may be incorporated into a non-natural amino acid polypeptide.

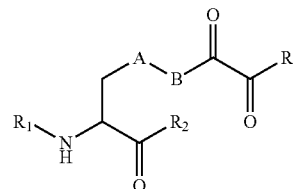
In addition to monocarbonyl structures, the non-natural amino acids described herein may include groups such as dicarbonyl, dicarbonyl like, masked dicarbonyl and protected dicarbonyl groups.

For example, the following amino acids having the structure of Formula (XI) are included:

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(XI)

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wherein A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

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B is optional, and when present is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-, —S(O)_k— where k is 1, 2, or 3, —S(O)_k(alkylene or substituted alkylene)-, —C(O)—, —C(O)-(alkylene or substituted alkylene)-, —C(S)—, —C(S)-(alkylene or substituted alkylene)-, —N(R')-, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')-, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')-, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O-, —S(O)_kN(R')-, —N(R')C(O)N(R')-, —N(R')C(S)N(R')-, —N(R')S(O)_kN(R')-, —N(R')—N=, —C(R')=N-, —C(R')=N—N(R')-, —C(R')=N—N=, —C(R')₂—N=N-, and —C(R')₂—N(R')—N(R')-, where each R' is independently H, alkyl, or substituted alkyl;

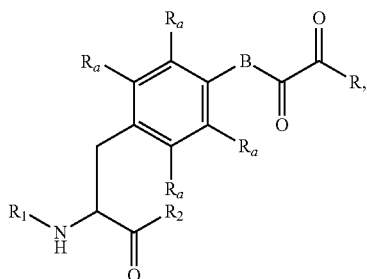
63

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide.

In addition, the following amino acids having the structure of Formula (XII) are included:



(XII)

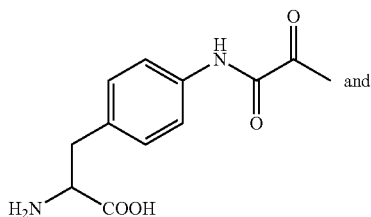
B is optional, and when present is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-, —S(O)_k— where k is 1, 2, or 3, —S(O)_k(alkylene or substituted alkylene)-, —C(O)—, —C(O)-(alkylene or substituted alkylene)-, —C(S)—, —C(S)-(alkylene or substituted alkylene)-, —N(R')—, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')—, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')—, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O—, —S(O)_kN(R')—, —N(R')C(O)N(R')—, —N(R')C(S)N(R')—, —N(R')S(O)_kN(R')—, —N(R')—N=, —C(R')—N=, —C(R')=N—N(R')—, —C(R')=N—N=, —C(R')₂—N=N—, and —C(R')₂—N(R')—N(R')—, where each R' is independently H, alkyl, or substituted alkyl;

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

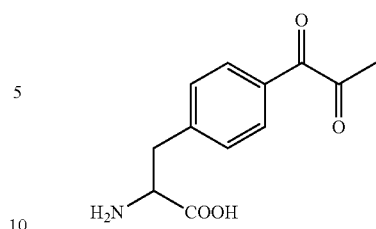
R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide; wherein each R_a is independently selected from the group consisting of H, halogen, alkyl, substituted alkyl, —N(R')₂, —C(O)_kR' where k is 1, 2, or 3, —C(O)N(R')₂, —OR', and —S(O)_kR', where each R' is independently H, alkyl, or substituted alkyl.

In addition, the following amino acids are included:



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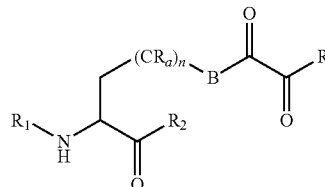
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wherein such compounds are optionally amino protected, optionally carboxyl protected, optionally amino protected and carboxyl protected, or a salt thereof. In addition, these non-natural amino acids and any of the following non-natural amino acids may be incorporated into a non-natural amino acid polypeptide.

In addition, the following amino acids having the structure of Formula (XIII) are included:

(XIII)



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wherein B is optional, and when present is a linker selected from the group consisting of lower alkylene, substituted lower alkylene, lower alkenylene, substituted lower alkenylene, lower heteroalkylene, substituted lower heteroalkylene, —O—, —O-(alkylene or substituted alkylene)-, —S—, —S-(alkylene or substituted alkylene)-, —S(O)_k— where k is 1, 2, or 3, —S(O)_k(alkylene or substituted alkylene)-, —C(O)—, —C(O)-(alkylene or substituted alkylene)-, —C(S)—, —C(S)-(alkylene or substituted alkylene)-, —N(R')—, —NR'-(alkylene or substituted alkylene)-, —C(O)N(R')—, —CON(R')-(alkylene or substituted alkylene)-, —CSN(R')—, —CSN(R')-(alkylene or substituted alkylene)-, —N(R')CO-(alkylene or substituted alkylene)-, —N(R')C(O)O—, —S(O)_kN(R')—, —N(R')C(O)N(R')—, —N(R')C(S)N(R')—, —N(R')S(O)_kN(R')—, —N(R')—N=, —C(R')—N=, —C(R')=N—N(R')—, —C(R')=N—N=, —C(R')₂—N=N—, and —C(R')₂—N(R')—N(R')—, where each R' is independently H, alkyl, or substituted alkyl;

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

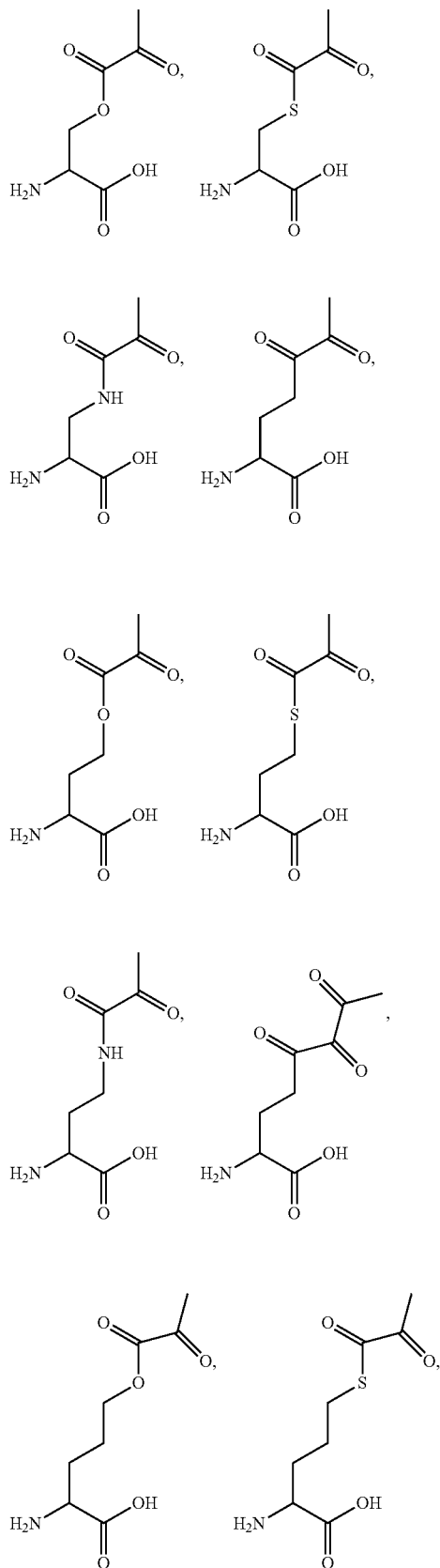
R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

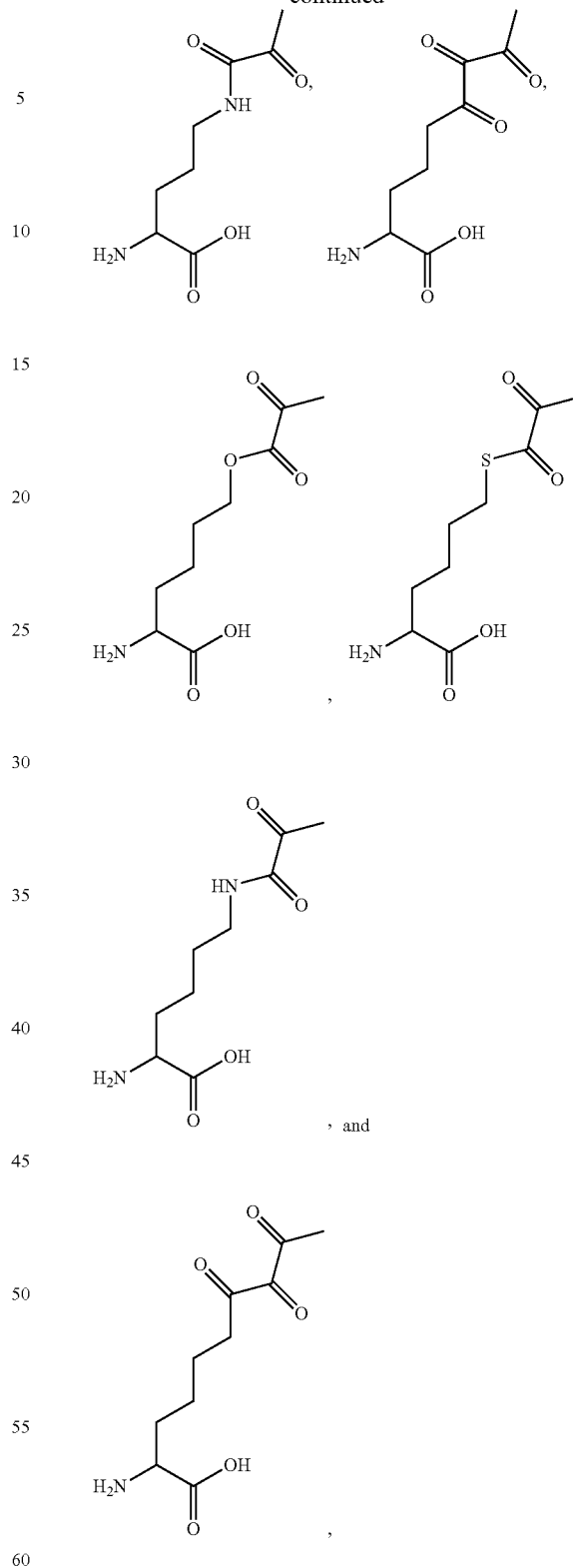
each R_a is independently selected from the group consisting of H, halogen, alkyl, substituted alkyl, —N(R')₂, —C(O)_kR' where k is 1, 2, or 3, —C(O)N(R')₂, —OR', and —S(O)_kR', where each R' is independently H, alkyl, or substituted alkyl; and n is 0 to 8.

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In addition, the following amino acids are included:

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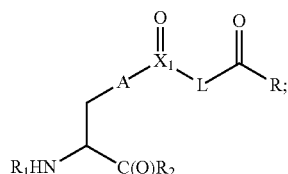
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wherein such compounds are optionally amino protected, optionally carboxyl protected, optionally amino protected and carboxyl protected, or a salt thereof. In addition, these non-natural amino acids and any of the following non-natural amino acids may be incorporated into a non-natural amino acid polypeptide.

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In addition, the following amino acids having the structure of Formula (XIV) are included:



(XIV) 5

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

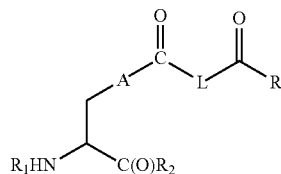
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

X₁ is C, S, or S(O); and L is alkylene, substituted alkylene, N(R')(alkylene) or N(R')(substituted alkylene), where R' is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl.

In addition, the following amino acids having the structure of Formula (XIV-A) are included:



(XIV-A) 40

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

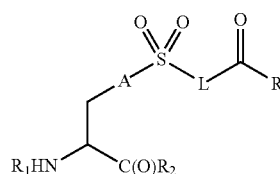
R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

L is alkylene, substituted alkylene, N(R')(alkylene) or N(R')(substituted alkylene), where R' is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl.

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In addition, the following amino acids having the structure of Formula (XIV-B) are included:



(XIV-B) 10

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

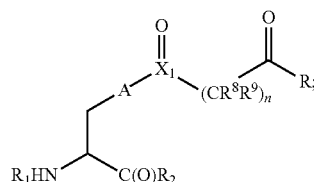
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

L is alkylene, substituted alkylene, N(R')(alkylene) or N(R')(substituted alkylene), where R' is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl.

In addition, the following amino acids having the structure of Formula (XV) are included:



(XV) 40

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

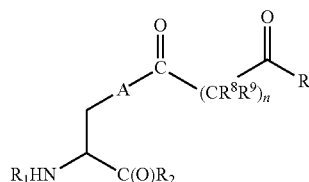
R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

X₁ is C, S, or S(O); and n is 0, 1, 2, 3, 4, or 5; and each R⁸ and R⁹ on each CR⁸R⁹ group is independently selected from the group consisting of H, alkoxy, alkylamine, halogen, alkyl, aryl, or any R⁸ and R⁹ can together form =O or a cycloalkyl, or any to adjacent R⁸ groups can together form a cycloalkyl.

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In addition, the following amino acids having the structure of Formula (XV-A) are included:



(XV-A) 5

wherein:

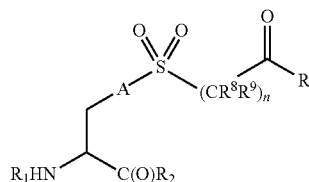
A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide; n is 0, 1, 2, 3, 4, or 5; and each R⁸ and R⁹ on each CR⁸R⁹ group is independently selected from the group consisting of H, alkoxy, alkylamine, halogen, alkyl, aryl, or any R⁸ and R⁹ can together form =O or a cycloalkyl, or any to adjacent R⁸ groups can together form a cycloalkyl.

In addition, the following amino acids having the structure of Formula (XV-B) are included:



(XV-B) 40

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

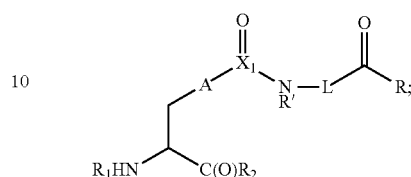
R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide; n is 0, 1, 2, 3, 4, or 5; and each R⁸ and R⁹ on each CR⁸R⁹ group is independently selected from the group consisting of H, alkoxy, alkylamine, halogen, alkyl, aryl, or any R⁸ and R⁹

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can together form =O or a cycloalkyl, or any to adjacent R⁸ groups can together form a cycloalkyl.

In addition, the following amino acids having the structure of Formula (XVI) are included:



(XVI)

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

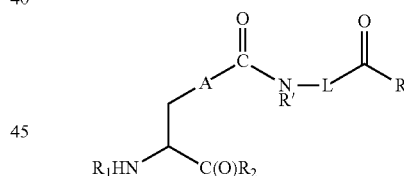
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

X₁ is C, S, or S(O); and L is alkylene, substituted alkylene, N(R')(alkylene) or N(R')(substituted alkylene), where R' is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl.

In addition, the following amino acids having the structure of Formula (XVI-A) are included:



(XVI-A)

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

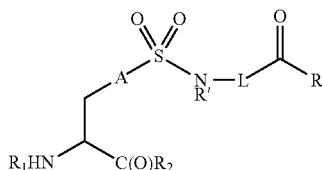
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide; L is alkylene, substituted alkylene, N(R')(alkylene) or N(R')(substituted alkylene), where R' is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl.

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In addition, the following amino acids having the structure of Formula (XVI-B) are included:



(XVI-B) 5

wherein:

A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

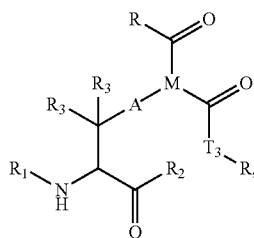
R is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

L is alkylene, substituted alkylene, N(R')(alkylene) or N(R')(substituted alkylene), where R' is H, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl.

In addition, amino acids having the structure of Formula (XVII) are included:

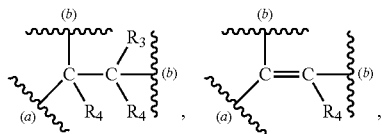


(XVII)

wherein:

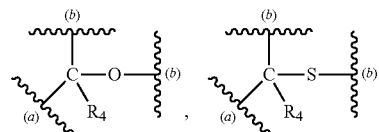
A is optional, and when present is lower alkylene, substituted lower alkylene, lower cycloalkylene, substituted lower cycloalkylene, lower alkenylene, substituted lower alkenylene, alkynylene, lower heteroalkylene, substituted heteroalkylene, lower heterocycloalkylene, substituted lower heterocycloalkylene, arylene, substituted arylene, heteroarylene, substituted heteroarylene, alkarylene, substituted alkarylene, aralkylene, or substituted aralkylene;

M is —C(R₃)—,

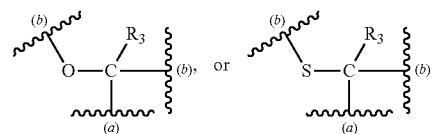
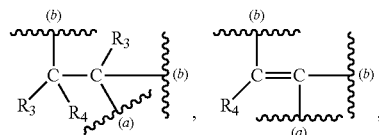


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where (a) indicates bonding to the A group and (b) indicates bonding to respective carbonyl groups, R₃ and R₄ are independently chosen from H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl, or R₃ and R₄ or two R₃ groups or two R₄ groups optionally form a cycloalkyl or a heterocycloalkyl;

R is H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

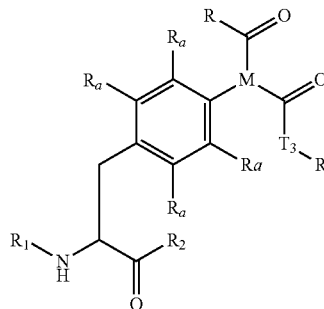
T₃ is a bond, C(R)(R), O, or S, and R is H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R₁ is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R₂ is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide.

In addition, amino acids having the structure of Formula (XVIII) are included:

(XVIII)



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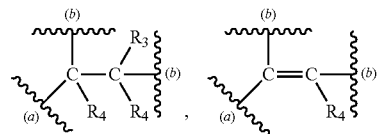
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wherein:

M is —C(R₃)—,

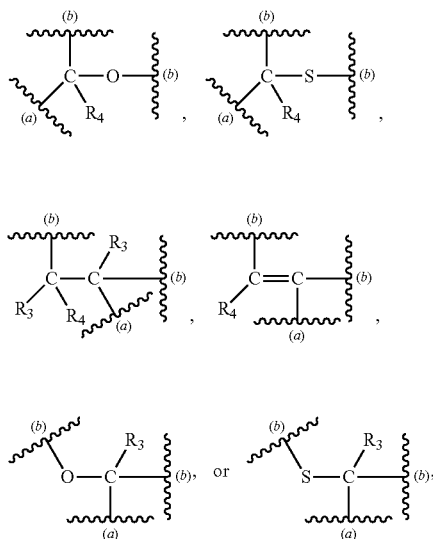
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where (a) indicates bonding to the A group and (b) indicates bonding to respective carbonyl groups, R_3 and R_4 are independently chosen from H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl, or R_3 and R_4 or two R_3 groups or two R_4 groups optionally form a cycloalkyl or a heterocycloalkyl;

R is H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

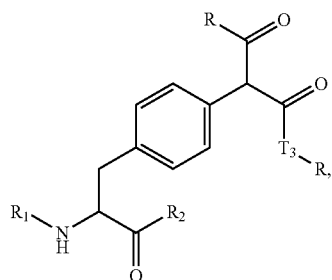
T_3 is a bond, $C(R)(R)$, O, or S, and R is H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl;

R_1 is optional, and when present, is H, an amino protecting group, resin, amino acid, polypeptide, or polynucleotide; and

R_2 is optional, and when present, is OH, an ester protecting group, resin, amino acid, polypeptide, or polynucleotide;

each R_a is independently selected from the group consisting of H, halogen, alkyl, substituted alkyl, $-N(R')_2$, $-C(O)_kR'$ where k is 1, 2, or 3, $-C(O)N(R')_2$, $-OR'$, and $-S(O)_kR'$, where each R' is independently H, alkyl, or substituted alkyl.

In addition, amino acids having the structure of Formula (XIX) are included:



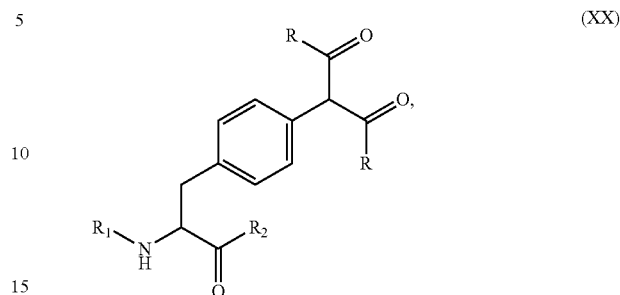
wherein:

R is H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl; and

T_3 is O, or S.

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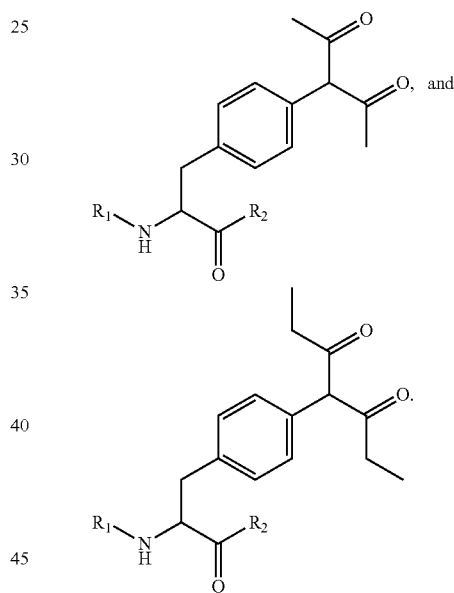
In addition, amino acids having the structure of Formula (XX) are included:



wherein:

R is H, halogen, alkyl, substituted alkyl, cycloalkyl, or substituted cycloalkyl.

In addition, the following amino acids having structures of Formula (XXI) are included:



In some embodiments, a polypeptide comprising a non-natural amino acid is chemically modified to generate a reactive carbonyl or dicarbonyl functional group. For instance, an aldehyde functionality useful for conjugation reactions can be generated from a functionality having adjacent amino and hydroxyl groups. Where the biologically active molecule is a polypeptide, for example, an N-terminal serine or threonine (which may be normally present or may be exposed via chemical or enzymatic digestion) can be used to generate an aldehyde functionality under mild oxidative cleavage conditions using periodate. See, e.g., Gaertner, et. al., Bioconjug. Chem. 3: 262-268 (1992); Geoghegan, K. & Stroh, J., Bioconjug. Chem. 3:138-146 (1992); Gaertner et al., J. Biol. Chem. 269:7224-7230 (1994). However, methods known in the art are restricted to the amino acid at the N-terminus of the peptide or protein.

In the present invention, a non-natural amino acid bearing adjacent hydroxyl and amino groups can be incorporated into the polypeptide as a "masked" aldehyde functionality. For

example, 5-hydroxylysine bears a hydroxyl group adjacent to the epsilon amine. Reaction conditions for generating the aldehyde typically involve addition of molar excess of sodium metaperiodate under mild conditions to avoid oxidation at other sites within the polypeptide. The pH of the oxidation reaction is typically about 7.0. A typical reaction involves the addition of about 1.5 molar excess of sodium meta periodate to a buffered solution of the polypeptide, followed by incubation for about 10 minutes in the dark. See, e.g. U.S. Pat. No. 6,423,685.

The carbonyl or dicarbonyl functionality can be reacted selectively with a hydroxylamine-containing reagent under mild conditions in aqueous solution to form the corresponding oxime linkage that is stable under physiological conditions. See, e.g., Jencks, W. P., *J. Am. Chem. Soc.* 81, 475-481 (1959); Shao, J. and Tam, J. P., *J. Am. Chem. Soc.* 117:3893-3899 (1995). Moreover, the unique reactivity of the carbonyl or dicarbonyl group allows for selective modification in the presence of the other amino acid side chains. See, e.g., Cornish, V. W., et al., *J. Am. Chem. Soc.* 118:8150-8151 (1996); Geoghegan, K. F. & Stroh, J. G., *Bioconjug. Chem.* 3:138-146 (1992); Mahal, L. K., et al., *Science* 276:1125-1128 (1997).

Structure and Synthesis of Non-natural Amino Acids: Hydroxylamine-containing Amino Acids

U.S. Provisional Patent Application No. 60/638,418 is incorporated by reference in its entirety. Thus, the disclosures provided in Section V (entitled "Non-natural Amino Acids"), Part B (entitled "Structure and Synthesis of Non-Natural Amino Acids: Hydroxylamine-Containing Amino Acids"), in U.S. Provisional Patent Application No. 60/638,418 apply fully to the methods, compositions (including Formulas I-XXXV), techniques and strategies for making, purifying, characterizing, and using non-natural amino acids, non-natural amino acid polypeptides and modified non-natural amino acid polypeptides described herein to the same extent as if such disclosures were fully presented herein. U.S. Patent Publication Nos. 2006/0194256, 2006/0217532, and 2006/0217289 and WO 2006/069246 entitled "Compositions containing, methods involving, and uses of non-natural amino acids and polypeptides," are also incorporated herein by reference in their entirety.

Chemical Synthesis of Unnatural Amino Acids

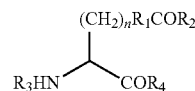
Many of the unnatural amino acids suitable for use in the present invention are commercially available, e.g., from Sigma (USA) or Aldrich (Milwaukee, Wis., USA). Those that are not commercially available are optionally synthesized as provided herein or as provided in various publications or using standard methods known to those of ordinary skill in the art. For organic synthesis techniques, see, e.g., *Organic Chemistry* by Fessenden and Fessenden, (1982, Second Edition, Willard Grant Press, Boston Mass.); *Advanced Organic Chemistry* by March (Third Edition, 1985, Wiley and Sons, New York); and *Advanced Organic Chemistry* by Carey and Sundberg (Third Edition, Parts A and B, 1990, Plenum Press, New York). Additional publications describing the synthesis of unnatural amino acids include, e.g., WO 2002/085923 entitled "In vivo incorporation of Unnatural Amino Acids;" Matsoukas et al., (1995) *J. Med. Chem.*, 38, 4660-4669; King, F. E. & Kidd, D. A. A. (1949) *A New Synthesis of Glutamine and of γ -Dipeptides of Glutamic Acid from Phthylated Intermediates*. *J. Chem. Soc.*, 3315-3319; Friedman, O. M. & Chatterji, R. (1959) *Synthesis of Derivatives of Glutamine as Model Substrates for Anti-Tumor Agents*. *J. Am. Chem. Soc.* 81, 3750-3752; Craig, J. C. et al. (1988) *Absolute Configuration of the Enantiomers of 7-Chloro-4 [[4-(diethylamino)-1-methylbutyl]amino]quinoline (Chloroquine)*. *J. Org. Chem.*

53, 1167-1170; Azoulay, M., Vilmont, M. & Frappier, F. (1991) *Glutamine analogues as Potential Antimalarials*, *Eur. J. Med. Chem.* 26, 201-5; Koskinen, A. M. P. & Rapoport, H. (1989) *Synthesis of 4-Substituted Prolines as Conformationally Constrained Amino Acid Analogues*. *J. Org. Chem.* 54, 1859-1866; Christie, B. D. & Rapoport, H. (1985) *Synthesis of Optically Pure Pípecolates from L-Asparagine. Application to the Total Synthesis of (+)-Apovincamine through Amino Acid Decarbonylation and Iminium Ion Cyclization*. *J. Org. Chem.* 50:1239-1246; Barton et al., (1987) *Synthesis of Novel α -Amino-Acids and Derivatives Using Radical Chemistry: Synthesis of L- and D- α -Amino-Adipic Acids, L- α -aminopimelic Acid and Appropriate Unsaturated Derivatives*. *Tetrahedron* 43:4297-4308; and, Subasinghe et al., (1992) *Quisqualic acid analogues: synthesis of beta-heterocyclic 2-aminopropanoic acid derivatives and their activity at a novel quisqualate-sensitized site*. *J. Med. Chem.* 35:4602-7. See also, U.S. Patent Publication No. US 2004/0198637 entitled "Protein Arrays," which is incorporated by reference herein.

A. Carbonyl Reactive Groups

Amino acids with a carbonyl reactive group allow for a variety of reactions to link molecules (including but not limited to, PEG or other water soluble molecules) via nucleophilic addition or aldol condensation reactions among others.

Exemplary carbonyl-containing amino acids can be represented as follows:



wherein n is 0-10; R₁ is an alkyl, aryl, substituted alkyl, or substituted aryl; R₂ is H, alkyl, aryl, substituted alkyl, and substituted aryl; and R₃ is H, an amino acid, a polypeptide, or an amino terminus modification group, and R₄ is H, an amino acid, a polypeptide, or a carboxy terminus modification group. In some embodiments, n is 1, R₁ is phenyl and R₂ is a simple alkyl (i.e., methyl, ethyl, or propyl) and the ketone moiety is positioned in the para position relative to the alkyl side chain. In some embodiments, n is 1, R₁ is phenyl and R₂ is a simple alkyl (i.e., methyl, ethyl, or propyl) and the ketone moiety is positioned in the meta position relative to the alkyl side chain.

The synthesis of p-acetyl-(+/-)-phenylalanine and m-acetyl-(+/-)-phenylalanine is described in Zhang, Z., et al., *Biochemistry* 42: 6735-6746 (2003), which is incorporated by reference herein. Other carbonyl-containing amino acids can be similarly prepared by one of ordinary skill in the art.

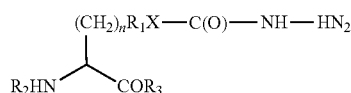
In some embodiments, a polypeptide comprising a non-naturally encoded amino acid is chemically modified to generate a reactive carbonyl functional group. For instance, an aldehyde functionality useful for conjugation reactions can be generated from a functionality having adjacent amino and hydroxyl groups. Where the biologically active molecule is a polypeptide, for example, an N-terminal serine or threonine (which may be normally present or may be exposed via chemical or enzymatic digestion) can be used to generate an aldehyde functionality under mild oxidative cleavage conditions using periodate. See, e.g., Gaertner, et *Bioconjug. Chem.* 3: 262-268 (1992); Geoghegan, K. & Stroh, J., *Bioconjug. Chem.* 3:138-146 (1992); Gaertner et al., *J. Biol. Chem.* 269:7224-7230 (1994). However, methods known in the art are restricted to the amino acid at the N-terminus of the peptide or protein.

In the present invention, a non-naturally encoded amino acid bearing adjacent hydroxyl and amino groups can be incorporated into the polypeptide as a "masked" aldehyde functionality. For example, 5-hydroxylysine bears a hydroxyl group adjacent to the epsilon amine. Reaction conditions for generating the aldehyde typically involve addition of molar excess of sodium metaperiodate under mild conditions to avoid oxidation at other sites within the polypeptide. The pH of the oxidation reaction is typically about 7.0. A typical reaction involves the addition of about 1.5 molar excess of sodium meta periodate to a buffered solution of the polypeptide, followed by incubation for about 10 minutes in the dark. See, e.g. U.S. Pat. No. 6,423,685, which is incorporated by reference herein.

The carbonyl functionality can be reacted selectively with a hydrazine-, hydrazide-, hydroxylamine-, or semicarbazide-containing reagent under mild conditions in aqueous solution to form the corresponding hydrazone, oxime, or semicarbazone linkages, respectively, that are stable under physiological conditions. See, e.g., Jencks, W. P., *J. Am. Chem. Soc.* 81, 475-481 (1959); Shao, J. and Tam, J. P., *J. Am. Chem. Soc.* 117:3893-3899 (1995). Moreover, the unique reactivity of the carbonyl group allows for selective modification in the presence of the other amino acid side chains. See, e.g., Cornish, V. W., et al., *J. Am. Chem. Soc.* 118:8150-8151 (1996); Geoghegan, K. F. & Stroh, J. G., *Bioconjug. Chem.* 3:138-146 (1992); Mahal, L. K., et al., *Science* 276:1125-1128 (1997).

B. Hydrazine, Hydrazide or Semicarbazide Reactive Groups
Non-naturally encoded amino acids containing a nucleophilic group, such as a hydrazine, hydrazide or semicarbazide, allow for reaction with a variety of electrophilic groups to form conjugates (including but not limited to, with PEG or other water soluble polymers).

Exemplary hydrazine, hydrazide or semicarbazide-containing amino acids can be represented as follows:



wherein n is 0-10; R₁ is an alkyl, aryl, substituted alkyl, or substituted aryl or not present; X is O, N, or S or not present; R₂ is H, an amino acid, a polypeptide, or an amino terminus modification group, and R₃ is H, an amino acid, a polypeptide, or a carboxy terminus modification group.

In some embodiments, n is 4, R₁ is not present, and X is N. In some embodiments, n is 2, R₁ is not present, and X is not present. In some embodiments, n is 1, R₁ is phenyl, X is O, and the oxygen atom is positioned para to the aliphatic group on the aryl ring.

Hydrazide-, hydrazine-, and semicarbazide-containing amino acids are available from commercial sources. For instance, L-glutamate-γ-hydrazide is available from Sigma Chemical (St. Louis, Mo.). Other amino acids not available commercially can be prepared by one of ordinary skill in the art. See, e.g., U.S. Pat. No. 6,281,211, which is incorporated by reference herein.

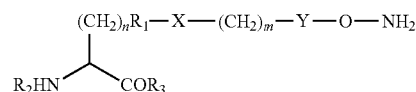
Polypeptides containing non-naturally encoded amino acids that bear hydrazide, hydrazine or semicarbazide functionalities can be reacted efficiently and selectively with a variety of molecules that contain aldehydes or other functional groups with similar chemical reactivity. See, e.g., Shao, J. and Tam, J., *J. Am. Chem. Soc.* 117:3893-3899 (1995). The unique reactivity of hydrazide, hydrazine and semicarbazide functional groups makes them significantly more reactive

toward aldehydes, ketones and other electrophilic groups as compared to the nucleophilic groups present on the 20 common amino acids (including but not limited to, the hydroxyl group of serine or threonine or the amino groups of lysine and the N-terminus).

C. Aminoxy-containing Amino Acids

Non-naturally encoded amino acids containing an aminoxy (also called a hydroxylamine) group allow for reaction with a variety of electrophilic groups to form conjugates (including but not limited to, with PEG or other water soluble polymers). Like hydrazines, hydrazides and semicarbazides, the enhanced nucleophilicity of the aminoxy group permits it to react efficiently and selectively with a variety of molecules that contain aldehydes or other functional groups with similar chemical reactivity. See, e.g., Shao, J. and Tam, J., *J. Am. Chem. Soc.* 117:3893-3899 (1995); H. Hang and C. Bertozzi, *Acc. Chem. Res.* 34: 727-736 (2001). Whereas the result of reaction with a hydrazine group is the corresponding hydrazone, however, an oxime results generally from the reaction of an aminoxy group with a carbonyl-containing group such as a ketone.

Exemplary amino acids containing aminoxy groups can be represented as follows:



wherein n is 0-10; R₁ is an alkyl, aryl, substituted alkyl, or substituted aryl or not present; X is O, N, S or not present; m is 0-10; Y=C(O) or not present; R₂ is H, an amino acid, a polypeptide, or an amino terminus modification group, and R₃ is H, an amino acid, a polypeptide, or a carboxy terminus modification group. In some embodiments, n is 1, R₁ is phenyl, X is O, m is 1, and Y is present. In some embodiments, n is 2, R₁ and X are not present, m is 0, and Y is not present.

Aminoxy-containing amino acids can be prepared from readily available amino acid precursors (homoserine, serine and threonine). See, e.g., M. Carrasco and R. Brown, *J. Org. Chem.* 68: 8853-8858 (2003). Certain aminoxy-containing amino acids, such as L-2-amino-4-(aminoxy)butyric acid, have been isolated from natural sources (Rosenthal, G., *Life Sci.* 60: 1635-1641 (1997). Other aminoxy-containing amino acids can be prepared by one of ordinary skill in the art.

D. Azide and Alkyne Reactive Groups

The unique reactivity of azide and alkyne functional groups makes them extremely useful for the selective modification of polypeptides and other biological molecules. Organic azides, particularly aliphatic azides, and alkynes are generally stable toward common reactive chemical conditions. In particular, both the azide and the alkyne functional groups are inert toward the side chains (i.e., R groups) of the 20 common amino acids found in naturally-occurring polypeptides. When brought into close proximity, however, the "spring-loaded" nature of the azide and alkyne groups is revealed and they react selectively and efficiently via Huisgen [3+2] cycloaddition reaction to generate the corresponding triazole. See, e.g., Chin J., et al., *Science* 301:964-7 (2003); Wang, Q., et al., *J. Am. Chem. Soc.* 125, 3192-3193 (2003); Chin, J. W., et al., *J. Am. Chem. Soc.* 124:9026-9027 (2002).

Because the Huisgen cycloaddition reaction involves a selective cycloaddition reaction (see, e.g., Padwa, A., in *COMPREHENSIVE ORGANIC SYNTHESIS*, Vol. 4, (ed. Trost, B. M., 1991), p. 1069-1109; Huisgen, R. in *1,3-DIPOLAR CYCLOADDITION CHEMISTRY*, (ed. Padwa, A., 1984), p. 1-176) rather than a

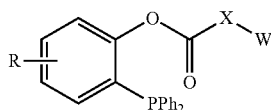
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nucleophilic substitution, the incorporation of non-naturally encoded amino acids bearing azide and alkyne-containing side chains permits the resultant polypeptides to be modified selectively at the position of the non-naturally encoded amino acid. Cycloaddition reaction involving azide or alkyne-containing hPP polypeptide can be carried out at room temperature under aqueous conditions by the addition of Cu(II) (including but not limited to, in the form of a catalytic amount of CuSO₄) in the presence of a reducing agent for reducing Cu(II) to Cu(I), in situ, in catalytic amount. See, e.g., Wang, Q., et al., *J. Am. Chem. Soc.* 125, 3192-3193 (2003); Tornøe, C. W., et al., *J. Org. Chem.* 67:3057-3064 (2002); Rostovtsev, et al., *Angew. Chem. Int. Ed.* 41:2596-2599 (2002). Exemplary reducing agents include, including but not limited to, ascorbate, metallic copper, quinine, hydroquinone, vitamin K, glutathione, cysteine, Fe²⁺, Co²⁺, and an applied electric potential.

In some cases, where a Huisgen [3+2] cycloaddition reaction between an azide and an alkyne is desired, the hPP polypeptide comprises a non-naturally encoded amino acid comprising an alkyne moiety and the water soluble polymer to be attached to the amino acid comprises an azide moiety. Alternatively, the converse reaction (i.e., with the azide moiety on the amino acid and the alkyne moiety present on the water soluble polymer) can also be performed.

The azide functional group can also be reacted selectively with a water soluble polymer containing an aryl ester and appropriately functionalized with an aryl phosphine moiety to generate an amide linkage. The aryl phosphine group reduces the azide in situ and the resulting amine then reacts efficiently with a proximal ester linkage to generate the corresponding amide. See, e.g., E. Saxon and C. Bertozzi, *Science* 287, 2007-2010 (2000). The azide-containing amino acid can be either an alkyl azide (including but not limited to, 2-amino-6-azido-1-hexanoic acid) or an aryl azide (p-azido-phenylalanine).

Exemplary water soluble polymers containing an aryl ester and a phosphine moiety can be represented as follows:

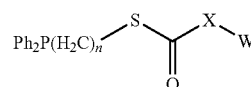


wherein X can be O, N, S or not present, Ph is phenyl, W is a water soluble polymer and R can be H, alkyl, aryl, substituted alkyl and substituted aryl groups. Exemplary R groups include but are not limited to —CH₂—, —C(CH₃)₃—, —OR', —NR'R'', —SR', —halogen, —C(O)R', —CONR'R'', —S(O)₂R', —S(O)₂NR'R'', —CN and —NO₂. R', R'', R''' and R'''' each independently refer to hydrogen, substituted or unsubstituted heteroalkyl, substituted or unsubstituted aryl, including but not limited to, aryl substituted with 1-3 halogens, substituted or unsubstituted alkyl, alkoxy or thioalkoxy groups, or arylalkyl groups. When a compound of the invention includes more than one R group, for example, each of the R groups is independently selected as are each R', R'', R''' and R'''' groups when more than one of these groups is present. When R' and R'' are attached to the same nitrogen atom, they can be combined with the nitrogen atom to form a 5-, 6-, or 7-membered ring. For example, —NR'R'' is meant to include, but not be limited to, 1-pyrrolidinyl and 4-morpholinyl. From the above discussion of substituents, one of skill in the art will understand that the term “alkyl” is meant to include groups including carbon atoms bound to groups other than hydrogen

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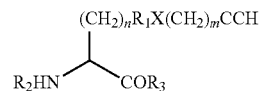
groups, such as haloalkyl (including but not limited to, —CF₃ and —CH₂CF₃) and acyl (including but not limited to, —C(O)CH₃, —C(O)CF₃, —C(O)CH₂OCH₃, and the like).

The azide functional group can also be reacted selectively with a water soluble polymer containing a thioester and appropriately functionalized with an aryl phosphine moiety to generate an amide linkage. The aryl phosphine group reduces the azide in situ and the resulting amine then reacts efficiently with the thio ester linkage to generate the corresponding amide. Exemplary water soluble polymers containing a thioester and a phosphine moiety can be represented as follows:



wherein n is 1-10; X can be O, N, S or not present, Ph is phenyl, and W is a water soluble polymer.

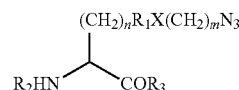
Exemplary alkyne-containing amino acids can be represented as follows:



wherein n is 0-10; R₁ is an alkyl, aryl, substituted alkyl, or substituted aryl or not present; X is O, N, S or not present; m is 0-10, R₂ is H, an amino acid, a polypeptide, or an amino terminus modification group, and R₃ is H, an amino acid, a polypeptide, or a carboxy terminus modification group. In some embodiments, n is 1, R₁ is phenyl, X is not present, m is 0 and the acetylene moiety is positioned in the para position relative to the alkyl side chain. In some embodiments, n is 1, R₁ is phenyl, X is O, m is 1 and the propargyloxy group is positioned in the para position relative to the alkyl side chain (i.e., O-propargyl-tyrosine). In some embodiments, n is 1, R₁ and X are not present and m is 0 (i.e., propargylglycine).

Alkyne-containing amino acids are commercially available. For example, propargylglycine is commercially available from Peptech (Burlington, Mass.). Alternatively, alkyne-containing amino acids can be prepared according to standard methods. For instance, p-propargyloxyphenylalanine can be synthesized, for example, as described in Deiters, A., et al., *J. Am. Chem. Soc.* 125: 11782-11783 (2003), and 4-alkynyl-L-phenylalanine can be synthesized as described in Kayser, B., et al., *Tetrahedron* 53(7): 2475-2484 (1997). Other alkyne-containing amino acids can be prepared by one of ordinary skill in the art.

Exemplary azide-containing amino acids can be represented as follows:



wherein n is 0-10; R₁ is an alkyl, aryl, substituted alkyl, substituted aryl or not present; X is O, N, S or not present; m is 0-10; R₂ is H, an amino acid, a polypeptide, or an amino terminus modification group, and R₃ is H, an amino acid, a polypeptide, or a carboxy terminus modification group. In

some embodiments, n is 1, R_1 is phenyl, X is not present, m is 0 and the azide moiety is positioned para to the alkyl side chain. In some embodiments, n is 0-4 and R_1 and X are not present, and $m=0$. In some embodiments, n is 1, R_1 is phenyl, X is O, m is 2 and the β -azidoethoxy moiety is positioned in the para position relative to the alkyl side chain.

Azide-containing amino acids are available from commercial sources. For instance, 4-azidophenylalanine can be obtained from Chem-Impex International, Inc. (Wood Dale, Ill.). For those azide-containing amino acids that are not commercially available, the azide group can be prepared relatively readily using standard methods known to those of ordinary skill in the art, including but not limited to, via displacement of a suitable leaving group (including but not limited to, halide, mesylate, tosylate) or via opening of a suitably protected lactone. See, e.g., *Advanced Organic Chemistry* by March (Third Edition, 1985, Wiley and Sons, New York).

E. Amino-thiol Reactive Groups

The unique reactivity of beta-substituted amino-thiol functional groups makes them extremely useful for the selective modification of polypeptides and other biological molecules that contain aldehyde groups via formation of the thiazolidine. See, e.g., J. Shao and J. Tam, *J. Am. Chem. Soc.* 1995, 117 (14) 3893-3899. In some embodiments, beta-substituted amino-thiol amino acids can be incorporated into hPP polypeptides and then reacted with water soluble polymers comprising an aldehyde functionality. In some embodiments, a water soluble polymer, drug conjugate or other payload can be coupled to an hPP polypeptide comprising a beta-substituted amino-thiol amino acid via formation of the thiazolidine.

F. Additional Reactive Groups

Additional reactive groups and non-naturally encoded amino acids, including but not limited to para-amino-phenylalanine, that can be incorporated into hPP or hA or hFc of the invention are described in the following patent applications which are all incorporated by reference in their entirety herein: U.S. Patent Publication No. 2006/0194256, U.S. Patent Publication No. 2006/0217532, U.S. Patent Publication No. 2006/0217289, U.S. Provisional Patent No. 60/755,338; U.S. Provisional Patent No. 60/755,711; U.S. Provisional Patent No. 60/755,018; International Patent Application No. PCT/US06/49397; WO 2006/069246; U.S. Provisional Patent No. 60/743,041; U.S. Provisional Patent No. 60/743,040; International Patent Application No. PCT/US06/47822; U.S. Provisional Patent No. 60/882,819; U.S. Provisional Patent No. 60/882,500; and U.S. Provisional Patent No. 60/870,594. These applications also discuss reactive groups that may be present on PEG or other polymers, including but not limited to, hydroxylamine (aminoxy) groups for conjugation.

Cellular Uptake of Unnatural Amino Acids

Unnatural amino acid uptake by a cell is one issue that is typically considered when designing and selecting unnatural amino acids, including but not limited to, for incorporation into a protein. For example, the high charge density of α -amino acids suggests that these compounds are unlikely to be cell permeable. Natural amino acids are taken up into the eukaryotic cell via a collection of protein-based transport systems. A rapid screen can be done which assesses which unnatural amino acids, if any, are taken up by cells. See, e.g., the toxicity assays in, e.g., U.S. Patent Publication No. US 2004/0198637 entitled "Protein Arrays" which is incorporated by reference herein; and Liu, D. R. & Schultz, P. G. (1999) *Progress toward the evolution of an organism with an expanded genetic code*. *PNAS United States* 96:4780-4785. Although uptake is easily analyzed with various assays, an alternative to designing unnatural amino acids that are ame-

nable to cellular uptake pathways is to provide biosynthetic pathways to create amino acids in vivo.

Biosynthesis of Unnatural Amino Acids

Many biosynthetic pathways already exist in cells for the production of amino acids and other compounds. While a biosynthetic method for a particular unnatural amino acid may not exist in nature, including but not limited to, in a cell, the invention provides such methods. For example, biosynthetic pathways for unnatural amino acids are optionally generated in host cell by adding new enzymes or modifying existing host cell pathways. Additional new enzymes are optionally naturally occurring enzymes or artificially evolved enzymes. For example, the biosynthesis of p-aminophenylalanine (as presented in an example in WO 2002/085923 entitled "In vivo incorporation of unnatural amino acids") relies on the addition of a combination of known enzymes from other organisms. The genes for these enzymes can be introduced into a eukaryotic cell by transforming the cell with a plasmid comprising the genes. The genes, when expressed in the cell, provide an enzymatic pathway to synthesize the desired compound. Examples of the types of enzymes that are optionally added are provided in the examples below. Additional enzymes sequences are found, for example, in Genbank. Artificially evolved enzymes are also optionally added into a cell in the same manner. In this manner, the cellular machinery and resources of a cell are manipulated to produce unnatural amino acids.

A variety of methods are available for producing novel enzymes for use in biosynthetic pathways or for evolution of existing pathways. For example, recursive recombination, including but not limited to, as developed by Maxygen, Inc. (available on the World Wide Web at maxygen.com), is optionally used to develop novel enzymes and pathways. See, e.g., Stemmer (1994), *Rapid evolution of a protein in vitro by DNA shuffling*, *Nature* 370(4):389-391; and, Stemmer, (1994), *DNA shuffling by random fragmentation and reassembly: In vitro recombination for molecular evolution*, *Proc. Natl. Acad. Sci. USA.*, 91:10747-10751. Similarly Design-Path™, developed by Genencor (available on the World Wide Web at genencor.com) is optionally used for metabolic pathway engineering, including but not limited to, to engineer a pathway to create O-methyl-L-tyrosine in a cell. This technology reconstructs existing pathways in host organisms using a combination of new genes, including but not limited to, those identified through functional genomics, and molecular evolution and design. Diversa Corporation (available on the World Wide Web at diversa.com) also provides technology for rapidly screening libraries of genes and gene pathways, including but not limited to, to create new pathways.

Typically, the unnatural amino acid produced with an engineered biosynthetic pathway of the invention is produced in a concentration sufficient for efficient protein biosynthesis, including but not limited to, a natural cellular amount, but not to such a degree as to affect the concentration of the other amino acids or exhaust cellular resources. Typical concentrations produced in vivo in this manner are about 10 mM to about 0.05 mM. Once a cell is transformed with a plasmid comprising the genes used to produce enzymes desired for a specific pathway and an unnatural amino acid is generated, in vivo selections are optionally used to further optimize the production of the unnatural amino acid for both ribosomal protein synthesis and cell growth.

Polypeptides with Unnatural Amino Acids

The incorporation of an unnatural amino acid can be done for a variety of purposes, including but not limited to, tailoring changes in protein structure and/or function, changing size, acidity, nucleophilicity, hydrogen bonding, hydropho-

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bicity, accessibility of protease target sites, targeting to a moiety (including but not limited to, for a protein array), adding a biologically active molecule, attaching a polymer, attaching a radionuclide, modulating serum half-life, modulating tissue penetration (e.g. tumors), modulating active transport, modulating tissue, cell or organ specificity or distribution, modulating immunogenicity, modulating protease resistance, etc. Proteins that include an unnatural amino acid can have enhanced or even entirely new catalytic or biophysical properties. For example, the following properties are optionally modified by inclusion of an unnatural amino acid into a protein: toxicity, biodistribution, structural properties, spectroscopic properties, chemical and/or photochemical properties, catalytic ability, half-life (including but not limited to, serum half-life), ability to react with other molecules, including but not limited to, covalently or noncovalently, and the like. The compositions including proteins that include at least one unnatural amino acid are useful for, including but not limited to, novel therapeutics, diagnostics, catalytic enzymes, industrial enzymes, binding proteins (including but not limited to, antibodies), and including but not limited to, the study of protein structure and function. See, e.g., Dougherty, (2000) *Unnatural Amino Acids as Probes of Protein Structure and Function*, *Current Opinion in Chemical Biology*, 4:645-652.

In one aspect of the invention, a composition includes at least one protein with at least one, including but not limited to, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten or more unnatural amino acids. The unnatural amino acids can be the same or different, including but not limited to, there can be 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more different sites in the protein that comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more different unnatural amino acids. In another aspect, a composition includes a protein with at least one, but fewer than all, of a particular amino acid present in the protein is substituted with the unnatural amino acid. For a given protein with more than one unnatural amino acids, the unnatural amino acids can be identical or different (including but not limited to, the protein can include two or more different types of unnatural amino acids, or can include two of the same unnatural amino acid). For a given protein with more than two unnatural amino acids, the unnatural amino acids can be the same, different or a combination of a multiple unnatural amino acid of the same kind with at least one different unnatural amino acid.

Proteins or polypeptides of interest with at least one unnatural amino acid are a feature of the invention. The invention also includes polypeptides or proteins with at least one unnatural amino acid produced using the compositions and methods of the invention. An excipient (including but not limited to, a pharmaceutically acceptable excipient) can also be present with the protein.

By producing proteins or polypeptides of interest with at least one unnatural amino acid in eukaryotic cells, proteins or polypeptides will typically include eukaryotic post-translational modifications. In certain embodiments, a protein includes at least one unnatural amino acid and at least one post-translational modification that is made in vivo by a eukaryotic cell, where the post-translational modification is not made by a prokaryotic cell. For example, the post-translational modification includes, including but not limited to, acetylation, acylation, lipid-modification, palmitoylation, palmitate addition, phosphorylation, glycolipid-linkage modification, glycosylation, and the like. In one aspect, the post-translational modification includes attachment of an oligosaccharide (including but not limited to, (GlcNAc-Man)₂-Man-GlcNAc-GlcNAc) to an asparagine by a GlcNAc-as-

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paragine linkage. See Table 1 which lists some examples of N-linked oligosaccharides of eukaryotic proteins (additional residues can also be present, which are not shown). In another aspect, the post-translational modification includes attachment of an oligosaccharide (including but not limited to, Gal-GalNAc, Gal-GlcNAc, etc.) to a serine or threonine by a GalNAc-serine or GalNAc-threonine linkage, or a GlcNAc-serine or a GlcNAc-threonine linkage.

TABLE 1

EXAMPLES OF OLIGOSACCHARIDES THROUGH GlcNAc-LINKAGE	
Type	Base Structure
High-mannose	$\begin{array}{c} \text{Man}\alpha 1-6 \\ \diagdown \quad \diagup \\ \text{Man}\alpha 1-3 \quad \text{Man}\alpha 1-6 \\ \quad \quad \quad \diagdown \quad \diagup \\ \quad \quad \quad \text{Man}\alpha 1-3 \quad \text{Man}\beta 1-4\text{GlcNAc}\beta 1-4\text{GlcNAc}\beta 1-\text{Asn} \end{array}$
Hybrid	$\begin{array}{c} \text{Man}\alpha 1-6 \\ \diagdown \quad \diagup \\ \text{GlcNAc}\beta 1-2-\text{Man}\alpha 1-3 \quad \text{Man}\beta 1-4\text{GlcNAc}\beta 1-4\text{GlcNAc}\beta 1-\text{Asn} \end{array}$
Complex	$\begin{array}{c} \text{GlcNAc}\beta 1-2-\text{Man}\alpha 1-6 \\ \diagdown \quad \diagup \\ \text{GlcNAc}\beta 1-2-\text{Man}\alpha 1-3 \quad \text{Man}\beta 1-4\text{GlcNAc}\beta 1-4\text{GlcNAc}\beta 1-\text{Asn} \end{array}$
Xylose	$\begin{array}{c} \text{Man}\alpha 1-6 \\ \diagdown \quad \diagup \\ \text{Xyl}\beta 1-2 \quad \text{Man}\beta 1-4\text{GlcNAc}\beta 1-4\text{GlcNAc}\beta 1-\text{Asn} \end{array}$

In yet another aspect, the post-translation modification includes proteolytic processing of precursors (including but not limited to, calcitonin precursor, calcitonin gene-related peptide precursor, preproparathyroid hormone, preproinsulin, proinsulin, prepro-opiomelanocortin, pro-opiomelanocortin and the like), assembly into a multisubunit protein or macromolecular assembly, translation to another site in the cell (including but not limited to, to organelles, such as the endoplasmic reticulum, the Golgi apparatus, the nucleus, lysosomes, peroxisomes, mitochondria, chloroplasts, vacuoles, etc., or through the secretory pathway). In certain embodiments, the protein comprises a secretion or localization sequence, an epitope tag, a FLAG tag, a polyhistidine tag, a GST fusion, or the like. U.S. Pat. Nos. 4,963,495 and 6,436,674, which are incorporated herein by reference, detail constructs that may improve secretion of hPP polypeptides.

One advantage of an unnatural amino acid is that it presents additional chemical moieties that can be used to add additional molecules. These modifications can be made in vivo in a eukaryotic or non-eukaryotic cell, or in vitro. Thus, in certain embodiments, the post-translational modification is through the unnatural amino acid. For example, the post-translational modification can be through a nucleophilic-electrophilic reaction. Most reactions currently used for the selective modification of proteins involve covalent bond formation between nucleophilic and electrophilic reaction partners, including but not limited to the reaction of α -haloketones with histidine or cysteine side chains. Selectivity in these cases is determined by the number and accessibility of the nucleophilic residues in the protein. In proteins of the invention, other more selective reactions can be used such as the reaction of an unnatural keto-amino acid with hydrazides or aminoxy compounds, in vitro and in vivo. See, e.g., Cornish,

et al., (1996) *J. Am. Chem. Soc.*, 118:8150-8151; Mahal, et al., (1997) *Science*, 276:1125-1128; Wang, et al., (2001) *Science* 292:498-500; Chin, et al., (2002) *J. Am. Chem. Soc.* 124:9026-9027; Chin, et al., (2002) *Proc. Natl. Acad. Sci.*, 99:11020-11024; Wang, et al., (2003) *Proc. Natl. Acad. Sci.*, 100:56-61; Zhang, et al., (2003) *Biochemistry*, 42:6735-6746; and, Chin, et al., (2003) *Science*, 301:964-7, all of which are incorporated by reference herein. This allows the selective labeling of virtually any protein with a host of reagents including fluorophores, crosslinking agents, saccharide derivatives and cytotoxic molecules. See also, U.S. Pat. No. 6,927,042 entitled "Glycoprotein synthesis," which is incorporated by reference herein. Post-translational modifications, including but not limited to, through an azido amino acid, can also be made through the Staudinger ligation (including but not limited to, with triarylphosphine reagents). See, e.g., Mick et al., (2002) *Incorporation of azides into recombinant proteins for chemoselective modification by the Staudinger ligation*, PNAS 99:19-24.

This invention provides another highly efficient method for the selective modification of proteins, which involves the genetic incorporation of unnatural amino acids, including but not limited to, containing an azide or alkynyl moiety into proteins in response to a selector codon. These amino acid side chains can then be modified by, including but not limited to, a Huisgen [3+2] cycloaddition reaction (see, e.g., Padwa, A. in *Comprehensive Organic Synthesis*, Vol. 4, (1991) Ed. Trost, B. M., Pergamon, Oxford, p. 1069-1109; and, Huisgen, R. in *1,3-Dipolar Cycloaddition Chemistry*, (1984) Ed. Padwa, A., Wiley, New York, p. 1-176) with, including but not limited to, alkynyl or azide derivatives, respectively. Because this method involves a cycloaddition rather than a nucleophilic substitution, proteins can be modified with extremely high selectivity. This reaction can be carried out at room temperature in aqueous conditions with excellent regioselectivity (1.4>1.5) by the addition of catalytic amounts of Cu(I) salts to the reaction mixture. See, e.g., Tomoe, et al., (2002) *J. Org. Chem.* 67:3057-3064; and, Rostovtsev, et al., (2002) *Angew. Chem. Int. Ed.* 41:2596-2599. Another method that can be used is the ligand exchange on a bisarsenic compound with a tetracysteine motif, see, e.g., Griffin, et al., (1998) *Science* 281:269-272.

A molecule that can be added to a protein of the invention through a [3+2] cycloaddition includes virtually any molecule with an azide or alkynyl derivative. Molecules include, but are not limited to, dyes, fluorophores, crosslinking agents, saccharide derivatives, polymers (including but not limited to, derivatives of polyethylene glycol), photocrosslinkers, cytotoxic compounds, affinity labels, derivatives of biotin, resins, beads, a second protein or polypeptide (or more), polynucleotide(s) (including but not limited to, DNA, RNA, etc.), metal chelators, cofactors, fatty acids, carbohydrates, and the like. These molecules can be added to an unnatural amino acid with an alkynyl group, including but not limited to, p-propargyloxyphenylalanine, or azido group, including but not limited to, p-azido-phenylalanine, respectively. V. In vivo Generation of hPP or hA or hFc Comprising Non-genetically-encoded Amino Acids

The hPP or hFc polypeptides of the invention can be generated in vivo using modified tRNA and tRNA synthetases to add to or substitute amino acids that are not encoded in naturally-occurring systems.

Methods for generating tRNAs and tRNA synthetases which use amino acids that are not encoded in naturally-occurring systems are described in, e.g., U.S. Pat. No. 7,045, 337 and U.S. Patent Application Publication 2003/0108885 (Ser. No. 10/126,931) which are incorporated by reference

herein. These methods involve generating a translational machinery that functions independently of the synthetases and tRNAs endogenous to the translation system (and are therefore sometimes referred to as "orthogonal"). Typically, the translation system comprises an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS). Typically, the O-RS preferentially aminoacylates the O-tRNA with at least one non-naturally occurring amino acid in the translation system and the O-tRNA recognizes at least one selector codon that is not recognized by other tRNAs in the system. The translation system thus inserts the non-naturally-encoded amino acid into a protein produced in the system, in response to an encoded selector codon, thereby "substituting" an amino acid into a position in the encoded polypeptide.

A wide variety of orthogonal tRNAs and aminoacyl tRNA synthetases have been described in the art for inserting particular synthetic amino acids into polypeptides, and are generally suitable for use in the present invention. For example, keto-specific O-tRNA/aminoacyl-tRNA synthetases are described in Wang, L., et al., *Proc. Natl. Acad. Sci. USA* 100:56-61 (2003) and Zhang, Z. et al., *Biochem.* 42(22): 6735-6746 (2003). Exemplary O-RS, or portions thereof, are encoded by polynucleotide sequences and include amino acid sequences disclosed in U.S. Patent Application Publications 2003/0082575 and 2003/0108885, each incorporated herein by reference. Corresponding O-tRNA molecules for use with the O-RSs are also described in U.S. Pat. No. 7,045,337 and U.S. Patent Application Publication 2003/0108885 (Ser. No. 10/126,931) which are incorporated by reference herein.

An example of an azide-specific O-tRNA/aminoacyl-tRNA synthetase system is described in Chin, J. W., et al., *J. Am. Chem. Soc.* 124:9026-9027 (2002). Exemplary O-RS sequences for p-azido-L-Phe include, but are not limited to, nucleotide sequences SEQ ID NOs: 14-16 and 29-32 and amino acid sequences SEQ ID NOs: 46-48 and 61-64 as disclosed in U.S. Patent Application Publication 2003/0108885 (Ser. No. 10/126,931) which is incorporated by reference herein. Exemplary O-tRNA sequences suitable for use in the present invention include, but are not limited to, nucleotide sequences SEQ ID NOs: 1-3 as disclosed in U.S. Patent Application Publication 2003/0108885 (Ser. No. 10/126,931) which is incorporated by reference herein. Other examples of O-tRNA/aminoacyl-tRNA synthetase pairs specific to particular non-naturally encoded amino acids are described in U.S. Pat. No. 7,045,337 which is incorporated by reference herein. O-RS and O-tRNA that incorporate both keto- and azide-containing amino acids in *S. cerevisiae* are described in Chin, J. W., et al, *Science* 301:964-967 (2003).

Several other orthogonal pairs have been reported. Glutaminyl (see, e.g., Liu, D. R., and Schultz, P. G. (1999) *Proc. Natl. Acad. Sci. U.S.A.* 96:4780-4785), aspartyl (see, e.g., Pasternak, M., et al., (2000) *Helv. Chim. Acta* 83:2277-2286), and tyrosyl (see, e.g., Ohno, S., et al., (1998) *J. Biochem. (Tokyo, Jpn.)* 124:1065-1068; and, Kowal, A. K., et al., (2001) *Proc. Natl. Acad. Sci. U.S.A.* 98:2268-2273) systems derived from *S. cerevisiae* tRNA's and synthetases have been described for the potential incorporation of unnatural amino acids in *E. coli*. Systems derived from the *E. coli* glutaminyl (see, e.g., Kowal, A. K., et al., (2001) *Proc. Natl. Acad. Sci. U.S.A.* 98:2268-2273) and tyrosyl (see, e.g., Edwards, H., and Schimmel, P. (1990) *Mol. Cell. Biol.* 10:1633-1641) synthetases have been described for use in *S. cerevisiae*. The *E. coli* tyrosyl system has been used for the incorporation of 3-iodo-L-tyrosine in vivo, in mammalian cells. See, Sakamoto, K., et al., (2002) *Nucleic Acids Res.* 30:4692-4699.

Use of O-tRNA/aminoacyl-tRNA synthetases involves selection of a specific codon which encodes the non-naturally encoded amino acid. While any codon can be used, it is generally desirable to select a codon that is rarely or never used in the cell in which the O-tRNA/aminoacyl-tRNA synthetase is expressed. For example, exemplary codons include nonsense codon such as stop codons (amber, ochre, and opal), four or more base codons and other natural three-base codons that are rarely or unused.

Specific selector codon(s) can be introduced into appropriate positions in the hPP polynucleotide coding sequence using mutagenesis methods known in the art (including but not limited to, site-specific mutagenesis, cassette mutagenesis, restriction selection mutagenesis, etc.).

Methods for generating components of the protein biosynthetic machinery, such as O-RSs, O-tRNAs, and orthogonal O-tRNA/O-RS pairs that can be used to incorporate a non-naturally encoded amino acid are described in Wang, L., et al., *Science* 292: 498-500 (2001); Chin, J. W., et al., *J. Am. Chem. Soc.* 124:9026-9027 (2002); Zhang, Z. et al., *Biochemistry* 42: 6735-6746 (2003). Methods and compositions for the in vivo incorporation of non-naturally encoded amino acids are described in U.S. Pat. No. 7,045,337, which is incorporated by reference herein. Methods for selecting an orthogonal tRNA-tRNA synthetase pair for use in in vivo translation system of an organism are also described in U.S. Pat. No. 7,045,337 and U.S. Patent Application Publication 2003/0108885 (Ser. No. 10/126,931) which are incorporated by reference herein. PCT Publication No. WO 04/035743 entitled "Site Specific Incorporation of Keto Amino Acids into Proteins," which is incorporated by reference herein in its entirety, describes orthogonal RS and tRNA pairs for the incorporation of keto amino acids. PCT Publication No. WO 04/094593 entitled "Expanding the Eukaryotic Genetic Code," which is incorporated by reference herein in its entirety, describes orthogonal RS and tRNA pairs for the incorporation of non-naturally encoded amino acids in eukaryotic host cells.

Methods for producing at least one recombinant orthogonal aminoacyl-tRNA synthetase (O-RS) comprise: (a) generating a library of (optionally mutant) RSs derived from at least one aminoacyl-tRNA synthetase (RS) from a first organism, including but not limited to, a prokaryotic organism, such as *Methanococcus jannaschii*, *Methanobacterium thermoautotrophicum*, *Halobacterium*, *Escherichia coli*, *A. fulgidus*, *P. furiosus*, *P. horikoshii*, *A. pernix*, *T. thermophilus*, or the like, or a eukaryotic organism; (b) selecting (and/or screening) the library of RSs (optionally mutant RSs) for members that aminoacylate an orthogonal tRNA (O-tRNA) in the presence of a non-naturally encoded amino acid and a natural amino acid, thereby providing a pool of active (optionally mutant) RSs; and/or, (c) selecting (optionally through negative selection) the pool for active RSs (including but not limited to, mutant RSs) that preferentially aminoacylate the O-tRNA in the absence of the non-naturally encoded amino acid, thereby providing the at least one recombinant O-RS; wherein the at least one recombinant O-RS preferentially aminoacylates the O-tRNA with the non-naturally encoded amino acid.

In one embodiment, the RS is an inactive RS. The inactive RS can be generated by mutating an active RS. For example, the inactive RS can be generated by mutating at least about 1, at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, or at least about 10 or more amino acids to different amino acids, including but not limited to, alanine.

Libraries of mutant RSs can be generated using various techniques known in the art, including but not limited to

rational design based on protein three dimensional RS structure, or mutagenesis of RS nucleotides in a random or rational design technique. For example, the mutant RSs can be generated by site-specific mutations, random mutations, diversity generating recombination mutations, chimeric constructs, rational design and by other methods described herein or known in the art.

In one embodiment, selecting (and/or screening) the library of RSs (optionally mutant RSs) for members that are active, including but not limited to, that aminoacylate an orthogonal tRNA (O-tRNA) in the presence of a non-naturally encoded amino acid and a natural amino acid, includes: introducing a positive selection or screening marker, including but not limited to, an antibiotic resistance gene, or the like, and the library of (optionally mutant) RSs into a plurality of cells, wherein the positive selection and/or screening marker comprises at least one selector codon, including but not limited to, an amber, ochre, or opal codon; growing the plurality of cells in the presence of a selection agent; identifying cells that survive (or show a specific response) in the presence of the selection and/or screening agent by suppressing the at least one selector codon in the positive selection or screening marker, thereby providing a subset of positively selected cells that contains the pool of active (optionally mutant) RSs. Optionally, the selection and/or screening agent concentration can be varied.

In one aspect, the positive selection marker is a chloramphenicol acetyltransferase (CAT) gene and the selector codon is an amber stop codon in the CAT gene. Optionally, the positive selection marker is a β -lactamase gene and the selector codon is an amber stop codon in the β -lactamase gene. In another aspect the positive screening marker comprises a fluorescent or luminescent screening marker or an affinity based screening marker (including but not limited to, a cell surface marker).

In one embodiment, negatively selecting or screening the pool for active RSs (optionally mutants) that preferentially aminoacylate the O-tRNA in the absence of the non-naturally encoded amino acid includes: introducing a negative selection or screening marker with the pool of active (optionally mutant) RSs from the positive selection or screening into a plurality of cells of a second organism, wherein the negative selection or screening marker comprises at least one selector codon (including but not limited to, an antibiotic resistance gene, including but not limited to, a chloramphenicol acetyltransferase (CAT) gene); and, identifying cells that survive or show a specific screening response in a first medium supplemented with the non-naturally encoded amino acid and a screening or selection agent, but fail to survive or to show the specific response in a second medium not supplemented with the non-naturally encoded amino acid and the selection or screening agent, thereby providing surviving cells or screened cells with the at least one recombinant O-RS. For example, a CAT identification protocol optionally acts as a positive selection and/or a negative screening in determination of appropriate O-RS recombinants. For instance, a pool of clones is optionally replicated on growth plates containing CAT (which comprises at least one selector codon) either with or without one or more non-naturally encoded amino acid. Colonies growing exclusively on the plates containing non-naturally encoded amino acids are thus regarded as containing recombinant O-RS. In one aspect, the concentration of the selection (and/or screening) agent is varied. In some aspects the first and second organisms are different. Thus, the first and/or second organism optionally comprises: a prokaryote, a eukaryote, a mammal, an *Escherichia coli*, a fungi, a yeast, an *archaeobacterium*, a *eubacterium*, a plant, an insect,

a protist, etc. In other embodiments, the screening marker comprises a fluorescent or luminescent screening marker or an affinity based screening marker.

In another embodiment, screening or selecting (including but not limited to, negatively selecting) the pool for active (optionally mutant) RSs includes: isolating the pool of active mutant RSs from the positive selection step (b); introducing a negative selection or screening marker, wherein the negative selection or screening marker comprises at least one selector codon (including but not limited to, a toxic marker gene, including but not limited to, a ribonuclease barnase gene, comprising at least one selector codon), and the pool of active (optionally mutant) RSs into a plurality of cells of a second organism; and identifying cells that survive or show a specific screening response in a first medium not supplemented with the non-naturally encoded amino acid, but fail to survive or show a specific screening response in a second medium supplemented with the non-naturally encoded amino acid, thereby providing surviving or screened cells with the at least one recombinant O-RS, wherein the at least one recombinant O-RS is specific for the non-naturally encoded amino acid. In one aspect, the at least one selector codon comprises about two or more selector codons. Such embodiments optionally can include wherein the at least one selector codon comprises two or more selector codons, and wherein the first and second organism are different (including but not limited to, each organism is optionally, including but not limited to, a prokaryote, a eukaryote, a mammal, an *Escherichia coli*, a fungi, a yeast, an archaeobacteria, a eubacteria, a plant, an insect, a protist, etc.). Also, some aspects include wherein the negative selection marker comprises a ribonuclease barnase gene (which comprises at least one selector codon). Other aspects include wherein the screening marker optionally comprises a fluorescent or luminescent screening marker or an affinity based screening marker. In the embodiments herein, the screenings and/or selections optionally include variation of the screening and/or selection stringency.

In one embodiment, the methods for producing at least one recombinant orthogonal aminoacyl-tRNA synthetase (O-RS) can further comprise: (d) isolating the at least one recombinant O-RS; (e) generating a second set of O-RS (optionally mutated) derived from the at least one recombinant O-RS; and, (f) repeating steps (b) and (c) until a mutated O-RS is obtained that comprises an ability to preferentially aminoacylate the O-tRNA. Optionally, steps (d)-(f) are repeated, including but not limited to, at least about two times. In one aspect, the second set of mutated O-RS derived from at least one recombinant O-RS can be generated by mutagenesis, including but not limited to, random mutagenesis, site-specific mutagenesis, recombination or a combination thereof.

The stringency of the selection/screening steps, including but not limited to, the positive selection/screening step (b), the negative selection/screening step (c) or both the positive and negative selection/screening steps (b) and (c), in the above-described methods, optionally includes varying the selection/screening stringency. In another embodiment, the positive selection/screening step (b), the negative selection/screening step (c) or both the positive and negative selection/screening steps (b) and (c) comprise using a reporter, wherein the reporter is detected by fluorescence-activated cell sorting (FACS) or wherein the reporter is detected by luminescence. Optionally, the reporter is displayed on a cell surface, on a phage display or the like and selected based upon affinity or catalytic activity involving the non-naturally encoded amino acid or an analogue. In one embodiment, the mutated synthetase is displayed on a cell surface, on a phage display or the like.

Methods for producing a recombinant orthogonal tRNA (O-tRNA) include: (a) generating a library of mutant tRNAs derived from at least one tRNA, including but not limited to, a suppressor tRNA, from a first organism; (b) selecting (including but not limited to, negatively selecting) or screening the library for (optionally mutant) tRNAs that are aminoacylated by an aminoacyl-tRNA synthetase (RS) from a second organism in the absence of a RS from the first organism, thereby providing a pool of tRNAs (optionally mutant); and, (c) selecting or screening the pool of tRNAs (optionally mutant) for members that are aminoacylated by an introduced orthogonal RS (O-RS), thereby providing at least one recombinant O-tRNA; wherein the at least one recombinant O-tRNA recognizes a selector codon and is not efficiently recognized by the RS from the second organism and is preferentially aminoacylated by the O-RS. In some embodiments the at least one tRNA is a suppressor tRNA and/or comprises a unique three base codon of natural and/or unnatural bases, or is a nonsense codon, a rare codon, an unnatural codon, a codon comprising at least 4 bases, an amber codon, an ochre codon, or an opal stop codon. In one embodiment, the recombinant O-tRNA possesses an improvement of orthogonality. It will be appreciated that in some embodiments, O-tRNA is optionally imported into a first organism from a second organism without the need for modification. In various embodiments, the first and second organisms are either the same or different and are optionally chosen from, including but not limited to, prokaryotes (including but not limited to, *Methanococcus jannaschii*, *Methanobacterium thermoautotrophicum*, *Escherichia coli*, *Halobacterium*, etc.), eukaryotes, mammals, fungi, yeasts, archaeobacteria, eubacteria, plants, insects, protists, etc. Additionally, the recombinant tRNA is optionally aminoacylated by a non-naturally encoded amino acid, wherein the non-naturally encoded amino acid is biosynthesized in vivo either naturally or through genetic manipulation. The non-naturally encoded amino acid is optionally added to a growth medium for at least the first or second organism.

In one aspect, selecting (including but not limited to, negatively selecting) or screening the library for (optionally mutant) tRNAs that are aminoacylated by an aminoacyl-tRNA synthetase (step (b)) includes: introducing a toxic marker gene, wherein the toxic marker gene comprises at least one of the selector codons (or a gene that leads to the production of a toxic or static agent or a gene essential to the organism wherein such marker gene comprises at least one selector codon) and the library of (optionally mutant) tRNAs into a plurality of cells from the second organism; and, selecting surviving cells, wherein the surviving cells contain the pool of (optionally mutant) tRNAs comprising at least one orthogonal tRNA or nonfunctional tRNA. For example, surviving cells can be selected by using a comparison ratio cell density assay.

In another aspect, the toxic marker gene can include two or more selector codons. In another embodiment of the methods, the toxic marker gene is a ribonuclease barnase gene, where the ribonuclease barnase gene comprises at least one amber codon. Optionally, the ribonuclease barnase gene can include two or more amber codons.

In one embodiment, selecting or screening the pool of (optionally mutant) tRNAs for members that are aminoacylated by an introduced orthogonal RS (O-RS) can include: introducing a positive selection or screening marker gene, wherein the positive marker gene comprises a drug resistance gene (including but not limited to, β -lactamase gene, comprising at least one of the selector codons, such as at least one amber stop codon) or a gene essential to the organism, or a

gene that leads to detoxification of a toxic agent, along with the O-RS, and the pool of (optionally mutant) tRNAs into a plurality of cells from the second organism; and, identifying surviving or screened cells grown in the presence of a selection or screening agent, including but not limited to, an antibiotic, thereby providing a pool of cells possessing the at least one recombinant tRNA, where the at least one recombinant tRNA is aminoacylated by the O-RS and inserts an amino acid into a translation product encoded by the positive marker gene, in response to the at least one selector codons. In another embodiment, the concentration of the selection and/or screening agent is varied.

Methods for generating specific O-tRNA/O-RS pairs are provided. Methods include: (a) generating a library of mutant tRNAs derived from at least one tRNA from a first organism; (b) negatively selecting or screening the library for (optionally mutant) tRNAs that are aminoacylated by an aminoacyl-tRNA synthetase (RS) from a second organism in the absence of a RS from the first organism, thereby providing a pool of (optionally mutant) tRNAs; (c) selecting or screening the pool of (optionally mutant) tRNAs for members that are aminoacylated by an introduced orthogonal RS (O-RS), thereby providing at least one recombinant O-tRNA. The at least one recombinant O-tRNA recognizes a selector codon and is not efficiently recognized by the RS from the second organism and is preferentially aminoacylated by the O-RS. The method also includes (d) generating a library of (optionally mutant) RSs derived from at least one aminoacyl-tRNA synthetase (RS) from a third organism; (e) selecting or screening the library of mutant RSs for members that preferentially aminoacylate the at least one recombinant O-tRNA in the presence of a non-naturally encoded amino acid and a natural amino acid, thereby providing a pool of active (optionally mutant) RSs; and, (f) negatively selecting or screening the pool for active (optionally mutant) RSs that preferentially aminoacylate the at least one recombinant O-tRNA in the absence of the non-naturally encoded amino acid, thereby providing the at least one specific O-tRNA/O-RS pair, wherein the at least one specific O-tRNA/O-RS pair comprises at least one recombinant O-RS that is specific for the non-naturally encoded amino acid and the at least one recombinant O-tRNA. Specific O-tRNA/O-RS pairs produced by the methods are included. For example, the specific OARNAs/O-RS pair can include, including but not limited to, a mutRNA^{Tyr}-mutTyrRS pair, such as a mutRNA^{Tyr}-SS12TyrRS pair, a mutRNA^{Leu}-mutLeuRS pair, a mutRNA^{Thr}-mutThrRS pair, a mutRNA^{Glu}-mutGluRS pair, or the like. Additionally, such methods include wherein the first and third organism are the same (including but not limited to, *Methanococcus jannaschii*).

Methods for selecting an orthogonal tRNA-tRNA synthetase pair for use in an in vivo translation system of a second organism are also included in the present invention. The methods include: introducing a marker gene, a tRNA and an aminoacyl-tRNA synthetase (RS) isolated or derived from a first organism into a first set of cells from the second organism; introducing the marker gene and the tRNA into a duplicate cell set from a second organism; and, selecting for surviving cells in the first set that fail to survive in the duplicate cell set or screening for cells showing a specific screening response that fail to give such response in the duplicate cell set, wherein the first set and the duplicate cell set are grown in the presence of a selection or screening agent, wherein the surviving or screened cells comprise the orthogonal tRNA-tRNA synthetase pair for use in the in vivo translation system of the second organism. In one embodiment, compar-

ing and selecting or screening includes an in vivo complementation assay. The concentration of the selection or screening agent can be varied.

The organisms of the present invention comprise a variety of organism and a variety of combinations. For example, the first and the second organisms of the methods of the present invention can be the same or different. In one embodiment, the organisms are optionally a prokaryotic organism, including but not limited to, *Methanococcus jannaschii*, *Methanobacterium thermoautotrophicum*, *Halobacterium*, *Escherichia coli*, *A. fulgidus*, *P. furiosus*, *P. horikoshii*, *A. permix*, *T. thermophilus*, or the like. Alternatively, the organisms optionally comprise a eukaryotic organism, including but not limited to, plants (including but not limited to, complex plants such as monocots, or dicots), algae, protists, fungi (including but not limited to, yeast, etc), animals (including but not limited to, mammals, insects, arthropods, etc.), or the like. In another embodiment, the second organism is a prokaryotic organism, including but not limited to, *Methanococcus jannaschii*, *Methanobacterium thermoautotrophicum*, *Halobacterium*, *Escherichia coli*, *A. fulgidus*, *Halobacterium*, *P. furiosus*, *P. horikoshii*, *A. permix*, *T. thermophilus*, or the like. Alternatively, the second organism can be a eukaryotic organism, including but not limited to, a yeast, a animal cell, a plant cell, a fungus, a mammalian cell, or the like. In various embodiments the first and second organisms are different.

VI. Location of Non-naturally-occurring Amino Acids in hPP or hFc

The present invention contemplates incorporation of one or more non-naturally-occurring amino acids into hPP or hFc polypeptides. One or more non-naturally-occurring amino acids may be incorporated at a particular position which does not disrupt activity of the polypeptide. This can be achieved by making "conservative" substitutions, including but not limited to, substituting hydrophobic amino acids with hydrophobic amino acids, bulky amino acids for bulky amino acids, hydrophilic amino acids for hydrophilic amino acids and/or inserting the non-naturally-occurring amino acid in a location that is not required for activity.

A variety of biochemical and structural approaches can be employed to select the desired sites for substitution with a non-naturally encoded amino acid within the hPP or hFc polypeptide. It is readily apparent to those of ordinary skill in the art that any position of the polypeptide chain is suitable for selection to incorporate a non-naturally encoded amino acid, and selection may be based on rational design or by random selection for any or no particular desired purpose. Selection of desired sites may be for producing an hPP or hFc molecule having any desired property or activity, including but not limited to, agonists, super-agonists, inverse agonists, antagonists, receptor binding modulators, receptor activity modulators, modulators of binding to binding partners, binder partner activity modulators, binding partner conformation modulators, dimer or multimer formation, no change to activity or property compared to the native molecule, or manipulating any physical or chemical property of the polypeptide such as solubility, aggregation, or stability. For example, locations in the polypeptide required for biological activity of hPP or hFc polypeptides can be identified using point mutation analysis, alanine scanning or homolog scanning methods known in the art. U.S. Pat. Nos. 5,580,723; 5,834,250; 6,013,478; 6,428,954; and 6,451,561, which are incorporated by reference herein, describe methods for the systematic analysis of the structure and function of polypeptides such as hGH by identifying active domains which influence the activity of the polypeptide with a target substance. Residues other than those identified as critical to biological activity by alanine or

homolog scanning mutagenesis may be good candidates for substitution with a non-naturally encoded amino acid depending on the desired activity sought for the polypeptide. Alternatively, the sites identified as critical to biological activity may also be good candidates for substitution with a non-naturally encoded amino acid, again depending on the desired activity sought for the polypeptide. Another alternative would be to simply make serial substitutions in each position on the polypeptide chain with a non-naturally encoded amino acid and observe the effect on the activities of the polypeptide. It is readily apparent to those of ordinary skill in the art that any means, technique, or method for selecting a position for substitution with a non-natural amino acid into any polypeptide is suitable for use in the present invention.

The structure and activity of naturally-occurring mutants of hPP polypeptides that contain deletions can also be examined to determine regions of the protein that are likely to be tolerant of substitution with a non-naturally encoded amino acid. Once residues that are likely to be intolerant to substitution with non-naturally encoded amino acids have been eliminated, the impact of proposed substitutions at each of the remaining positions can be examined from the three-dimensional crystal structure of the hPP or hFc and its binding proteins. Models may be made investigating the secondary and tertiary structure of polypeptides, if three-dimensional structural data is not available. Thus, those of ordinary skill in the art can readily identify amino acid positions that can be substituted with non-naturally encoded amino acids.

In sonic embodiments, the hPP or hFc polypeptides of the invention comprise one or more non-naturally occurring amino acids positioned in a region of the protein that does not disrupt the secondary structure of the polypeptide.

In some embodiments, one or more non-naturally encoded amino acids are incorporated at any position in one or more of the following regions corresponding to secondary structures in hA as follows: before position 1 (i.e. at the N-terminus), 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581, and after position 582 (i.e., at the carboxyl terminus of the protein), (SEQ ID NO: 1).

A wide variety of non-naturally encoded amino acids can be substituted for, or incorporated into, a given position in an hPP or hFc polypeptide. In general, a particular non-naturally encoded amino acid is selected for incorporation based on an examination of the three dimensional crystal structure of an hPP or hFc polypeptide with its receptor or binding partner, a preference for conservative substitutions (i.e., aryl-based non-naturally encoded amino acids, such as p-acetylphenylalanine or O-propargyltyrosine substituting for Phe, Tyr or Trp), and the specific conjugation chemistry that one desires to introduce into the hPP or hFc polypeptide (e.g., the introduction of 4-azidophenylalanine if one wants to effect a Huisgen [3+2] cycloaddition with a water soluble polymer bearing an alkyne moiety or a amide bond formation with a water soluble polymer that bears an aryl ester that, in turn, incorporates a phosphine moiety).

In one embodiment, the method further includes incorporating into the protein the unnatural amino acid, where the unnatural amino acid comprises a first reactive group; and contacting the protein with a molecule (including but not limited to, a label, a dye, a polymer, a water-soluble polymer, a derivative of polyethylene glycol, a photocrosslinker, a radionuclide, a cytotoxic compound, a drug, an affinity label, a photoaffinity label, a reactive compound, a resin, a second

protein or polypeptide or polypeptide analog, an antibody or antibody fragment, a metal chelator, a cofactor, a fatty acid, a carbohydrate, a polynucleotide, a DNA, a RNA, an antisense polynucleotide, a saccharide, a water-soluble dendrimer, a cyclodextrin, an inhibitory ribonucleic acid, a biomaterial, a nanoparticle, a spin label, a fluorophore, a metal-containing moiety, a radioactive moiety, a novel functional group, a group that covalently or noncovalently interacts with other molecules, a photocaged moiety, an actinic radiation excitable moiety, a photoisomerizable moiety, biotin, a derivative of biotin, a biotin analogue, a moiety incorporating a heavy atom, a chemically cleavable group, a photocleavable group, an elongated side chain, a carbon-linked sugar, a redox-active agent, an amino thioacid, a toxic moiety, an isotopically labeled moiety, a biophysical probe, a phosphorescent group, a chemiluminescent group, an electron dense group, a magnetic group, an intercalating group, a chromophore, an energy transfer agent, a biologically active agent, a detectable label, a small molecule, a quantum dot, a nanotransmitter, a radionucleotide, a radiotransmitter, a neutron-capture agent, or any combination of the above, or any other desirable compound or substance) that comprises a second reactive group. The first reactive group reacts with the second reactive group to attach the molecule to the unnatural amino acid through a [3+2] cycloaddition. In one embodiment, the first reactive group is an alkynyl or azido moiety and the second reactive group is an azido or alkynyl moiety. For example, the first reactive group is the alkynyl moiety (including but not limited to, in unnatural amino acid p-propargyloxyphenylalanine) and the second reactive group is the azido moiety. In another example, the first reactive group is the azido moiety (including but not limited to, in the unnatural amino acid p-azido-L-phenylalanine) and the second reactive group is the alkynyl moiety.

In some cases, the non-naturally encoded amino acid substitution(s) will be combined with other additions, substitutions or deletions within the hPP polypeptide to affect other biological traits of the hPP or hFc polypeptide. In some cases, the other additions, substitutions or deletions may increase the stability (including but not limited to, resistance to proteolytic degradation) of the hPP or hFc polypeptide or increase affinity of the hPP or hFc polypeptide for its receptor or binding partner. In some cases, the other additions, substitutions or deletions may increase the solubility (including but not limited to, when expressed in *E. coli* or other host cells) of the hPP or hFc polypeptide. In some embodiments additions, substitutions or deletions may increase the polypeptide solubility following expression in *E. coli* or other recombinant host cells. In some embodiments sites are selected for substitution with a naturally encoded or non-natural amino acid in addition to another site for incorporation of a non-natural amino acid that results in increasing the polypeptide solubility following expression in *E. coli* or other recombinant host cells. In some embodiments, the hPP or hFc polypeptides comprise another addition, substitution or deletion that modulates affinity for the hPP or hFc polypeptide receptor, binding proteins, or associated ligand, modulates (including but not limited to, increases or decreases) receptor dimerization, stabilizes receptor dimers, modulates circulating half-life, modulates release or bio-availability, facilitates purification, or improves or alters a particular route of administration. Similarly, hPP or hFc polypeptides can comprise chemical or enzyme cleavage sequences, protease cleavage sequences, reactive groups, antibody-binding domains (including but not limited to, FLAG or poly-His) or other affinity based sequences (including, but not limited to, FLAG, poly-His, GST, etc.) or linked molecules (including, but not limited to, biotin) that improve detection (including, but not limited to,

GFP), purification, transport through tissues or cell membranes, prodrug release or activation, hPP or hFc size reduction, or other traits of the polypeptide.

In some cases, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more amino acids are substituted with one or more non-naturally-encoded amino acids. In some cases, the hPP or hFc polypeptide further includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more substitutions of one or more non-naturally encoded amino acids for naturally-occurring amino acids. For example, in some embodiments, one or more residues in the following regions of hA are substituted with one or more non-naturally encoded amino acids: before position 1 (i.e. at the N-terminus), 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581, and after position 582 (i.e., at the carboxyl terminus of the protein),. (SEQ ID NO: 1).

In some cases, the one or more non-naturally encoded residues are linked to one or more lower molecular weight linear or branched PEGs (approximately ~5-20 kDa in mass or less), thereby enhancing binding affinity and comparable serum half-life relative to the species attached to a single, higher molecular weight PEG.

Preferred sites for incorporation in hA of two or more non-naturally encoded amino acids include combinations of the following residues: before position 1 (i.e. at the N-terminus), 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581, and after position 582 (i.e., at the carboxyl terminus of the protein),. (SEQ ID NO: 1).

VII. Expression in Non-eukaryotes and Eukaryotes

To obtain high level expression of a cloned hPP or hA or hFc polynucleotide, one typically subclones polynucleotides encoding an hPP or hA or hFc polypeptide of the invention into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable bacterial promoters are known to those of ordinary skill in the art and described, e.g., in Sambrook et al. and Ausubel et al. Bacterial expression systems for expressing hPP or hA or hFc polypeptides of the invention are available in, including but not limited to, *E. coli*, *Bacillus* sp., *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, and *Salmonella* (Palva et al., *Gene* 22:229-235 (1983); Mosbach et al., *Nature* 302:543-545 (1983)). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are known to those of ordinary skill in the art and are also commercially available. In cases where orthogonal tRNAs and aminoacyl tRNA synthetases (described above) are used to express the hPP or hA polypeptides of the invention, host cells for expression are selected based on their ability to use the orthogonal components. Exemplary host cells include Gram-positive bacteria (including but not limited to *B. brevis*, *B. subtilis*, or *Streptomyces*) and Gram-negative bacteria (*E. coli*, *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Pseudomonas putida*), as well as yeast and other eukaryotic cells. Cells comprising O-tRNA/O-RS pairs can be used as described herein.

A eukaryotic host cell or non-eukaryotic host cell of the present invention provides the ability to synthesize proteins that comprise unnatural amino acids in large useful quantities. In one aspect, the composition optionally includes,

including but not limited to, at least 10 micrograms, at least 50 micrograms, at least 75 micrograms, at least 100 micrograms, at least 200 micrograms, at least 250 micrograms, at least 500 micrograms, at least 1 milligram, at least 10 milligrams, at least 100 milligrams, at least one gram, or more of the protein that comprises an unnatural amino acid, or an amount that can be achieved with in vivo protein production methods (details on recombinant protein production and purification are provided herein). In another aspect, the protein is optionally present in the composition at a concentration of, including but not limited to, at least 10 micrograms of protein per liter, at least 50 micrograms of protein per liter, at least 75 micrograms of protein per liter, at least 100 micrograms of protein per liter, at least 200 micrograms of protein per liter, at least 250 micrograms of protein per liter, at least 500 micrograms of protein per liter, at least 1 milligram of protein per liter, or at least 10 milligrams of protein per liter or more, in, including but not limited to, a cell lysate, a buffer, a pharmaceutical buffer, or other liquid suspension (including but not limited to, in a volume of, including but not limited to, anywhere from about 1 nl to about 100 L or more). The production of large quantities (including but not limited to, greater than that typically possible with other methods, including but not limited to, in vitro translation) of a protein in a eukaryotic cell including at least one unnatural amino acid is a feature of the invention.

A eukaryotic host cell or non-eukaryotic host cell of the present invention provides the ability to biosynthesize proteins that comprise unnatural amino acids in large useful quantities. For example, proteins comprising an unnatural amino acid can be produced at a concentration of, including but not limited to, at least 10 µg/liter, at least 50 µg/liter, at least 75 µg/liter, at least 100 µg/liter, at least 200 µg/liter, at least 250 µg/liter, or at least 500 µg/liter, at least 1 mg/liter, at least 2 mg/liter, at least 3 mg/liter, at least 4 mg/liter, at least 5 mg/liter, at least 6 mg/liter, at least 7 mg/liter, at least 8 mg/liter, at least 9 mg/liter, at least 10 mg/liter, at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900 mg/liter, 1g/liter, 5 g/liter, 10 g/liter or more of protein in a cell extract, cell lysate, culture medium, a buffer, and/or the like.

A number of vectors suitable for expression of hPP or hFc are commercially available. Useful expression vectors for eukaryotic hosts, include but are not limited to, vectors comprising expression control sequences from SV40, bovine papilloma virus, adenovirus and cytomegalovirus. Such vectors include pcDNA3.1(+)\Hyg (Invitrogen, Carlsbad, Calif., USA) and pCI-neo (Stratagene, La Jolla, Calif., USA). Bacterial plasmids, such as plasmids from *E. coli*, including pBR322, pET3a and pET12a, wider host range plasmids, such as RP4, phage DNAs, e.g., the numerous derivatives of phage lambda, e.g., NM989, and other DNA phages, such as M13 and filamentous single stranded DNA phages may be used. The 2µ plasmid and derivatives thereof, the POT1 vector (U.S. Pat. No. 4,931,373 which is incorporated by reference), the pJSO37 vector described in (Okkels, Ann. New York Acad. Sci. 782, 202 207, 1996) and pPICZ A, B or C (Invitrogen) may be used with yeast host cells. For insect cells, the vectors include but are not limited to, pVL941, pBG311 (Cate et al., "Isolation of the Bovine and Human Genes for Mullerian Inhibiting Substance And Expression of the Human Gene In Animal Cells", Cell, 45, pp. 685 98 (1986), pBluebac 4.5 and pMelbac (Invitrogen, Carlsbad, Calif.).

The nucleotide sequence encoding a hPP or hFc polypeptide may or may not also include sequence that encodes a signal peptide. The signal peptide is present when the

polypeptide is to be secreted from the cells in which it is expressed. Such signal peptide may be any sequence. The signal peptide may be prokaryotic or eukaryotic. Coloma, M (1992) J. Imm. Methods 152:89-104 describe a signal peptide for use in mammalian cells (murine Ig kappa light chain signal peptide). Other signal peptides include but are not limited to, the α -factor signal peptide from *S. cerevisiae* (U.S. Pat. No. 4,870,008 which is incorporated by reference herein), the signal peptide of mouse salivary amylase (O. Hagenbuchle et al., Nature 289, 1981, pp. 643-646), a modified carboxypeptidase signal peptide (L. A. Valls et al., Cell 48, 1987, pp. 887-897), the yeast BAR1 signal peptide (WO 87/02670, which is incorporated by reference herein), and the yeast aspartic protease 3 (YAPS) signal peptide (cf. M. Egel-Mitani et al., Yeast 6, 1990, pp. 127-137).

Examples of suitable mammalian host cells are known to those of ordinary skill in the art. Such host cells may be Chinese hamster ovary (CHO) cells, (e.g. CHO-K1; ATCC CCL-61), Green Monkey cells (COS) (e.g. COS1 (ATCC CRL-1650), COS 7 (ATCC CRL-1651)); mouse cells (e.g. NS/O), Baby Hamster Kidney (BHK) cell lines (e.g. ATCC CRL-1632 or ATCC CCL-10), and human cells (e.g. HEK 293 (ATCC CRL-1573)), as well as plant cells in tissue culture. These cell lines and others are available from public depositories such as the American Type Culture Collection, Rockville, Md. In order to provide improved glycosylation of a hPP polypeptide, a mammalian host cell may be modified to express sialyltransferase, e.g. 1,6-sialyltransferase, e.g. as described in U.S. Pat. No. 5,047,335, which is incorporated by reference herein.

Methods for the introduction of exogenous DNA into mammalian host cells include but are not limited to, calcium phosphate-mediated transfection, electroporation, DEAE-dextran mediated transfection, liposome-mediated transfection, viral vectors and the transfection methods described by Life Technologies Ltd, Paisley, UK using Lipofectamine 2000 and Roche Diagnostics Corporation, Indianapolis, USA using FuGENE 6. These methods are well known in the art and are described by Ausbel et al. (eds.), 1996, Current Protocols in Molecular Biology, John Wiley & Sons, New York, USA. The cultivation of mammalian cells may be performed according to established methods, e.g. as disclosed in (Animal Cell Biotechnology, Methods and Protocols, Edited by Nigel Jenkins, 1999, Human Press Inc. Totowa, N.J., USA and Harrison Mass. and Rae I F, General Techniques of Cell Culture, Cambridge University Press 1997).

I. Expression Systems, Culture, and Isolation

hPP or hA or hFc polypeptides may be expressed in any number of suitable expression systems including, for example, yeast, insect cells, mammalian cells, and bacteria. A description of exemplary expression systems is provided below.

Yeast As used herein, the term "yeast" includes any of the various yeasts capable of expressing a gene encoding an hPP or hA or hFc polypeptide. Such yeasts include, but are not limited to, ascosporogenous yeasts (Endomycetales), basidiomycetous yeasts and yeasts belonging to the Fungi imperfecti (Blastomycetes) group. The ascosporogenous yeasts are divided into two families, Sporophthoraceae and Saccharomycetaceae. The latter is comprised of four subfamilies, Schizosaccharomycoidae (e.g., genus *Schizosaccharomyces*), Nadsonioideae, Lipomycoideae and Saccharomycoideae (e.g., genera *Pichia*, *Kluyveromyces* and *Saccharomyces*). The basidiomycetous yeasts include the genera *Leucosporidium*, *Rhodospiridium*, *Sporidiobolus*, *Filobasidium*, and *Filobasidiella*. Yeasts belonging to the Fungi Imperfecti (Blastomycetes) group are divided into two

families, Sporobolomycetaceae (e.g., genera *Sporobolomyces* and *Bullera*) and Cryptococcaceae (e.g., genus *Candida*).

Of particular interest for use with the present invention are species within the genera *Pichia*, *Kluyveromyces*, *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*, *Torulopsis*, and *Candida*, including, but not limited to, *P. pastoris*, *P. guilliermondii*, *S. cerevisiae*, *S. carlsbergensis*, *S. diastaticus*, *S. douglasii*, *S. kluyveri*, *S. norbensis*, *S. oviformis*, *K. lactis*, *K. fragilis*, *C. albicans*, *C. maltosa*, and *H. polymorpha*.

The selection of suitable yeast for expression of hPP or hA or hFc polypeptides is within the skill of one of ordinary skill in the art. In selecting yeast hosts for expression, suitable hosts may include those shown to have, for example, good secretion capacity, low proteolytic activity, good secretion capacity, good soluble protein production, and overall robustness. Yeast are generally available from a variety of sources including, but not limited to, the Yeast Genetic Stock Center, Department of Biophysics and Medical Physics, University of California (Berkeley, Calif.), and the American Type Culture Collection ("ATCC") (Manassas, Va.).

The term "yeast host" or "yeast host cell" includes yeast that can be, or has been, used as a recipient for recombinant vectors or other transfer DNA. The term includes the progeny of the original yeast host cell that has received the recombinant vectors or other transfer DNA. It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement to the original parent, due to accidental or deliberate mutation. Progeny of the parental cell that are sufficiently similar to the parent to be characterized by the relevant property, such as the presence of a nucleotide sequence encoding an hPP or hA polypeptide, are included in the progeny intended by this definition.

Expression and transformation vectors, including extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeast hosts. For example, expression vectors have been developed for *S. cerevisiae* (Sikorski et al., GENETICS (1989) 122:19; Ito et al., J. BACTERIOL. (1983) 153:163; Hinnen et al., PROC. NATL. ACAD. SCI. USA (1978) 75:1929; *C. albicans* (Kurtz et al., MOL. CELL. BIOL. (1986) 6:142); *C. maltosa* (Kunze et al., J. BASIC MICROBIOL. (1985) 25:141); *H. polymorpha* (Gleeson et al., J. GEN. MICROBIOL. (1986) 132:3459; Roggenkamp et al., MOL. GENETICS AND GENOMICS (1986) 202:302); *K. fragilis* (Das et al., J. BACTERIOL. (1984) 158:1165); *K. lactis* (De Louvencourt et al., J. BACTERIOL. (1983) 154:737; Van den Berg et al., BIOTECHNOLOGY (NY) (1990) 8:135); *P. guilliermondii* (Kunze et al., J. BASIC MICROBIOL. (1985) 25:141); *P. pastoris* (U.S. Pat. Nos. 5,324,639; 4,929,555; and 4,837,148; Cregg et al., MOL. CELL. BIOL. (1985) 5:3376); *Schizosaccharomyces pombe* (Beach et al., NATURE (1982) 300:706); and *Y. lipolytica*; *A. nidulans* (Ballance et al., BIOCHEM. BIOPHYS. RES. COMMUN. (1983) 112:284-89; Tilburn et al., GENE (1983) 26:205-221; and Yelton et al., PROC. NATL. ACAD. SCI. USA (1984) 81:1470-74); *A. niger* (Kelly and Hynes, EMBO J. (1985) 4:475-479); *T. reesia* (EP 0 244 234); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357), each incorporated by reference herein.

Control sequences for yeast vectors are known to those of ordinary skill in the art and include, but are not limited to, promoter regions from genes such as alcohol dehydrogenase (ADH) (EP 0 284 044); enolase; glucokinase; glucose-6-phosphate isomerase; glyceraldehyde-3-phosphate dehydrogenase (GAP or GAPDH); hexokinase; phosphofructokinase; 3-phosphoglycerate mutase; and pyruvate kinase (PyK) (EP 0 329 203). The yeast PHO5 gene, encoding acid phosphatase, also may provide useful promoter sequences (Miy-

anohara et al., PROC. NATL. ACAD. SCI. USA (1983) 80:1). Other suitable promoter sequences for use with yeast hosts may include the promoters for 3-phosphoglycerate kinase (Hitzeman et al., J. BIOL. CHEM. (1980) 255:12073); and other glycolytic enzymes, such as pyruvate decarboxylase, triose-phosphate isomerase, and phosphoglucose isomerase (Holland et al., BIOCHEMISTRY (1978) 17:4900; Hess et al., J. ADV. ENZYME REG. (1969) 7:149). Inducible yeast promoters having the additional advantage of transcription controlled by growth conditions may include the promoter regions for alcohol dehydrogenase 2; isocytichrome C; acid phosphatase; metallothionein; glyceraldehyde-3-phosphate dehydrogenase; degradative enzymes associated with nitrogen metabolism; and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 0 073 657.

Yeast enhancers also may be used with yeast promoters. In addition, synthetic promoters may also function as yeast promoters. For example, the upstream activating sequences (UAS) of a yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region. See U.S. Pat. Nos. 4,880,734 and 4,876,197, which are incorporated by reference herein. Other examples of hybrid promoters include promoters that consist of the regulatory sequences of the ADH2, GAL4, GAL10, or PHO5 genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK. See EP 0 164 556. Furthermore, a yeast promoter may include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription.

Other control elements that may comprise part of the yeast expression vectors include terminators, for example, from GAPDH or the enolase genes (Holland et al., J. BIOL. CHEM. (1981) 256:1385). In addition, the origin of replication from the 2 μ plasmid origin is suitable for yeast. A suitable selection gene for use in yeast is the trp1 gene present in the yeast plasmid. See Tschumper et al., GENE (1980) 10:157; Kingsman et al., GENE (1979) 7:141. The trp1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan. Similarly, Leu2-deficient yeast strains (ATCC 20,622 or 38,626) are complemented by known plasmids bearing the Leu gene.

Methods of introducing exogenous DNA into yeast hosts are known to those of ordinary skill in the art, and typically include, but are not limited to, either the transformation of spheroplasts or of intact yeast host cells treated with alkali cations. For example, transformation of yeast can be carried out according to the method described in Hsiao et al., PROC. NATL. ACAD. SCI. USA (1979) 76:3829 and Van Solingen et al., J. BACT. (1977) 130:946. However, other methods for introducing DNA into cells such as by nuclear injection, electroporation, or protoplast fusion may also be used as described generally in SAMBROOK ET AL., MOLECULAR CLONING: A LAB. MANUAL (2001). Yeast host cells may then be cultured using standard techniques known to those of ordinary skill in the art.

Other methods for expressing heterologous proteins in yeast host cells are known to those of ordinary skill in the art. See generally U.S. Patent Publication No. 20020055169, U.S. Pat. Nos. 6,361,969; 6,312,923; 6,183,985; 6,083,723; 6,017,731; 5,674,706; 5,629,203; 5,602,034; and 5,089,398; U.S. Reexamined Patent Nos. RE37,343 and RE35,749; PCT Published Patent Applications WO 99/07862; WO 98/37208; and WO 98/26080; European Patent Applications EP 0 946 736; EP 0 732 403; EP 0 480 480; WO 90/10277; EP 0 340

986; EP 0 329 203; EP 0 324 274; and EP 0 164 556. See also Gellissen et al., ANTONIE VAN LEEUWENHOEK (1992) 62(1-2):79-93; Romanos et al., YEAST (1992) 8(6):423-488; Goeddel, METHODS IN ENZYMOLOGY (1990) 185:3-7, each incorporated by reference herein.

The yeast host strains may be grown in fermentors during the amplification stage using standard feed batch fermentation methods known to those of ordinary skill in the art. The fermentation methods may be adapted to account for differences in a particular yeast host's carbon utilization pathway or mode of expression control. For example, fermentation of a *Saccharomyces* yeast host may require a single glucose feed, complex nitrogen source (e.g., casein hydrolysates), and multiple vitamin supplementation. In contrast, the methylotrophic yeast *P. pastoris* may require glycerol, methanol, and trace mineral feeds, but only simple ammonium (nitrogen) salts for optimal growth and expression. See, e.g., U.S. Pat. No. 5,324,639; Elliott et al., J. PROTEIN CHEM. (1990) 9:95; and Fieschko et al., BIOTECH. BIOENG. (1987) 29:1113, incorporated by reference herein.

Such fermentation methods, however, may have certain common features independent of the yeast host strain employed. For example, a growth limiting nutrient, typically carbon, may be added to the fermentor during the amplification phase to allow maximal growth. In addition, fermentation methods generally employ a fermentation medium designed to contain adequate amounts of carbon, nitrogen, basal salts, phosphorus, and other minor nutrients (vitamins, trace minerals and salts, etc.). Examples of fermentation media suitable for use with *Pichia* are described in U.S. Pat. Nos. 5,324,639 and 5,231,178, which are incorporated by reference herein.

Baculovirus-Infected Insect Cells The term "insect host" or "insect host cell" refers to an insect that can be, or has been, used as a recipient for recombinant vectors or other transfer DNA. The term includes the progeny of the original insect host cell that has been transfected. It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement to the original parent, due to accidental or deliberate mutation. Progeny of the parental cell that are sufficiently similar to the parent to be characterized by the relevant property, such as the presence of a nucleotide sequence encoding an hPP or hA or hFc polypeptide, are included in the progeny intended by this definition.

The selection of suitable insect cells for expression of hPP or hA or hFc polypeptides is known to those of ordinary skill in the art. Several insect species are well described in the art and are commercially available including *Aedes aegypti*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni*. In selecting insect hosts for expression, suitable hosts may include those shown to have, inter alia, good secretion capacity, low proteolytic activity, and overall robustness. Insect are generally available from a variety of sources including, but not limited to, the Insect Genetic Stock Center, Department of Biophysics and Medical Physics, University of California (Berkeley, Calif.); and the American Type Culture Collection ("ATCC") (Manassas, Va.).

Generally, the components of a baculovirus-infected insect expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene to be expressed; a wild type baculovirus with sequences homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the bacu-

lovirus genome); and appropriate insect host cells and growth media. The materials, methods and techniques used in constructing vectors, transfecting cells, picking plaques, growing cells in culture, and the like are known in the art and manuals are available describing these techniques.

After inserting the heterologous gene into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, for example, Invitrogen Corp. (Carlsbad, Calif.). These techniques are generally known to those of ordinary skill in the art and fully described in SUMMERS AND SMITH, TEXAS AGRICULTURAL EXPERIMENT STATION BULLETIN No. 1555 (1987), herein incorporated by reference. See also, RICHARDSON, 39 METHODS IN MOLECULAR BIOLOGY: BACULOVIRUS EXPRESSION PROTOCOLS (1995); AUSUBEL ET AL., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY 16.9-16.11 (1994); KING AND POSSEE, THE BACULOVIRUS SYSTEM: A LABORATORY GUIDE (1992); and O'REILLY ET AL., BACULOVIRUS EXPRESSION VECTORS: A LABORATORY MANUAL (1992).

Indeed, the production of various heterologous proteins using baculovirus/insect cell expression systems is known to those of ordinary skill in the art. See, e.g., U.S. Pat. Nos. 6,368,825; 6,342,216; 6,338,846; 6,261,805; 6,245,528; 6,225,060; 6,183,987; 6,168,932; 6,126,944; 6,096,304; 6,013,433; 5,965,393; 5,939,285; 5,891,676; 5,871,986; 5,861,279; 5,858,368; 5,843,733; 5,762,939; 5,753,220; 5,605,827; 5,583,023; 5,571,709; 5,516,657; 5,290,686; WO 02/06305; WO 01/90390; WO 01/27301; WO 01/05956; WO 00/55345; WO 00/20032; WO 99/51721; WO 99/45130; WO 99/31257; WO 99/10515; WO 99/09193; WO 97/26332; WO 96/29400; WO 96/25496; WO 96/06161; WO 95/20672; WO 93/03173; WO 92/16619; WO 92/02628; WO 92/01801; WO 90/14428; WO 90/10078; WO 90/02566; WO 90/02186; WO 90/01556; WO 89/01038; WO 89/01037; WO 88/07082, which are incorporated by reference herein.

Vectors that are useful in baculovirus/insect cell expression systems are known in the art and include, for example, insect expression and transfer vectors derived from the baculovirus *Autographa californica* nuclear polyhedrosis virus (AcNPV), which is a helper-independent, viral expression vector. Viral expression vectors derived from this system usually use the strong viral polyhedrin gene promoter to drive expression of heterologous genes. See generally, O'Reilly ET AL., BACULOVIRUS EXPRESSION VECTORS: A LABORATORY MANUAL (1992).

Prior to inserting the foreign gene into the baculovirus genome, the above-described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are typically assembled into an intermediate transplacement construct (transfer vector). Intermediate transplacement constructs are often maintained in a replicon, such as an extra chromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification. More specifically, the plasmid may contain the polyhedrin polyadenylation signal (Miller, ANN. REV. MICROBIOL. (1988) 42:177) and a prokaryotic ampicillin-resistance (amp) gene and origin of replication for selection and propagation in *E. coli*.

One commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed including, for example, pVL985, which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI

cloning site 32 base pairs downstream from the ATT. See Luckow and Summers, VIROLOGY 170:31 (1989). Other commercially available vectors include, for example, PBlue-Bac4.5/V5-His; pBlueBacHis2; pMelBac; pBlueBac4.5 (Invitrogen Corp., Carlsbad, Calif.).

After insertion of the heterologous gene, the transfer vector and wild type baculoviral genome are co-transfected into an insect cell host. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. See SUMMERS AND SMITH, TEXAS AGRICULTURAL EXPERIMENT STATION BULLETIN No. 1555 (1987); Smith et al., MOL. CELL. BIOL. (1983) 3:2156; Luckow and Summers, VIROLOGY (1989) 170:31. For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. See Miller et al., BIOESSAYS (1989) 11(4):91.

Transfection may be accomplished by electroporation. See TROTTER AND WOOD, 39 METHODS IN MOLECULAR BIOLOGY (1995); Mann and King, J. GEN. VIROL. (1989) 70:3501. Alternatively, liposomes may be used to transfect the insect cells with the recombinant expression vector and the baculovirus. See, e.g., Liebman et al., BIOTECHNIQUES (1999) 26(1):36; Graves et al., BIOCHEMISTRY (1998) 37:6050; Nomura et al., J. BIOL. CHEM. (1998) 273(22):13570; Schmidt et al., PROTEIN EXPRESSION AND PURIFICATION (1998) 12:323; Siffert et al., NATURE GENETICS (1998) 18:45; TILKINS ET AL., CELL BIOLOGY: A LABORATORY HANDBOOK 145-154 (1998); Cai et al., PROTEIN EXPRESSION AND PURIFICATION (1997) 10:263; Dolphin et al., NATURE GENETICS (1997) 17:491; Kost et al., GENE (1997) 190:139; Jakobsson et al., J. BIOL. CHEM. (1996) 271:22203; Rowles et al., J. BIOL. CHEM. (1996) 271(37):22376; Reverey et al., J. BIOL. CHEM. (1996) 271(39):23607-10; Stanley et al., J. BIOL. CHEM. (1995) 270:4121; Sisk et al., J. VIROL. (1994) 68(2):766; and Peng et al., BIOTECHNIQUES (1993) 14(2):274. Commercially available liposomes include, for example, Cellfectin® and Lipofectin® (Invitrogen, Corp., Carlsbad, Calif.). In addition, calcium phosphate transfection may be used. See TROTTER AND WOOD, 39 METHODS IN MOLECULAR BIOLOGY (1995); Kitts, NAR (1990) 18(19):5667; and Mann and King, J. GEN. VIROL. (1989) 70:3501.

Baculovirus expression vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region typically includes an RNA polymerase binding site and a transcription initiation site. A baculovirus promoter may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Moreover, expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in the infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedrin protein (FRIESEN ET AL., *The Regulation of Baculovirus Gene Expression in The Molecular Biology of Baculoviruses* (1986); EP 0 127 839 and 0 155 476) and the gene encoding the p10 protein (Vlak et al., J. GEN. VIROL. (1988) 69:765).

The newly formed baculovirus expression vector is packaged into an infectious recombinant baculovirus and subsequently grown plaques may be purified by techniques known to those of ordinary skill in the art. See Miller et al., BIOESSAYS (1989) 11(4):91; SUMMERS AND SMITH, TEXAS AGRICULTURAL EXPERIMENT STATION BULLETIN No. 1555 (1987).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, inter alia, *Aedes aegypti* (ATCC No. CCL-125), *Bombyx mori* (ATCC No. CRL-8910), *Drosophila melanogaster* (ATCC No. 1963), *Spodoptera frugiperda*, and *Trichoplusia ni*. See Wright, NATURE (1986) 321:718; Carbonell et al., J. VIROL. (1985) 56:153; Smith et al., MOL. CELL. BIOL. (1983) 3:2156. See generally, Fraser et al., IN VITRO CELL. DEV. BIOL. (1989) 25:225. More specifically, the cell lines used for baculovirus expression vector systems commonly include, but are not limited to, Sf9 (*Spodoptera frugiperda*) (ATCC No. CRL-1711), Sf21 (*Spodoptera frugiperda*) (Invitrogen Corp., Cat. No. 11497-013 (Carlsbad, Calif.)), Tri-368 (*Trichoplusia ni*), and High-Five™ BTI-TN-5B1-4 (*Trichoplusia ni*).

Cells and culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression, and cell culture technology is generally known to those of ordinary skill in the art.

E. Coli, *Pseudomonas* species, and other Prokaryotes Bacterial expression techniques are known to those of ordinary skill in the art. A wide variety of vectors are available for use in bacterial hosts. The vectors may be single copy or low or high multicopy vectors. Vectors may serve for cloning and/or expression. In view of the ample literature concerning vectors, commercial availability of many vectors, and even manuals describing vectors and their restriction maps and characteristics, no extensive discussion is required here. As is well-known, the vectors normally involve markers allowing for selection, which markers may provide for cytotoxic agent resistance, prototrophy or immunity. Frequently, a plurality of markers is present, which provide for different characteristics.

A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region typically includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) [Raibaud et al., ANNU. REV. GENET. (1984) 18:173]. Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (lac) [Chang et al., NATURE (1977) 198:1056], and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (trp) [Goeddel et al., NUC. ACIDS RES. (1980) 8:4057; Yelverton et al., NUC. ACIDS RES. (1981) 9:731; U.S. Pat. No. 4,738,921; EP Pub. Nos. 036 776 and 121 775, which are incorporated by reference herein]. The β -ga-

lactosidase (bla) promoter system [Weissmann (1981) "The cloning of interferon and other mistakes." In Interferon 3 (Ed. I. Gresser)], bacteriophage lambda PL [Shimatake et al., NATURE (1981) 292:128] and T5 [U.S. Pat. No. 4,689,406, which are incorporated by reference herein] promoter systems also provide useful promoter sequences. Preferred methods of the present invention utilize strong promoters, such as the T7 promoter to induce hPP or hA polypeptides at high levels. Examples of such vectors are known to those of ordinary skill in the art and include the pET29 series from Novagen, and the pPOP vectors described in WO99/05297, which is incorporated by reference herein. Such expression systems produce high levels of hPP or hA or hFc polypeptides in the host without compromising host cell viability or growth parameters. pET19 (Novagen) is another vector known in the art.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter [U.S. Pat. No. 4,551,433, which is incorporated by reference herein]. For example, the tac promoter is a hybrid tip-lac promoter comprised of both tip promoter and lac operon sequences that is regulated by the lac repressor [Amann et al., GENE (1983) 25:167; de Boer et al., PROC. NATL. ACAD. SCI. (1983) 80:21]. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system [Studier et al., J. MOL. BIOL. (1986) 189:113; Tabor et al., Proc Natl. Acad. Sci. (1985) 82:1074]. In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EP Pub. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon [Shine et al., NATURE (1975) 254:34]. The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA [Steitz et al. "Genetic signals and nucleotide sequences in messenger RNA", In Biological Regulation and Development: Gene Expression (Ed. R. F. Goldberg, 1979)]. To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site [Sambrook et al. "Expression of cloned genes in *Escherichia coli*", Molecular Cloning: A Laboratory Manual, 1989].

The term "bacterial host" or "bacterial host cell" refers to a bacterial that can be, or has been, used as a recipient for recombinant vectors or other transfer DNA. The term includes the progeny of the original bacterial host cell that has been transfected. It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement to the original parent, due to accidental or deliberate mutation. Progeny of the parental cell that are sufficiently similar to the parent to be characterized by the relevant property, such as the

presence of a nucleotide sequence encoding an hPP or hA polypeptide, are included in the progeny intended by this definition.

The selection of suitable host bacteria for expression of hPP or hA polypeptides is known to those of ordinary skill in the art. In selecting bacterial hosts for expression, suitable hosts may include those shown to have, inter alia, good inclusion body formation capacity, low proteolytic activity, and overall robustness. Bacterial hosts are generally available from a variety of sources including, but not limited to, the Bacterial Genetic Stock Center, Department of Biophysics and Medical Physics, University of California (Berkeley, Calif.); and the American Type Culture Collection ("ATCC") (Manassas, Va.). Industrial/pharmaceutical fermentation generally use bacterial derived from K strains (e.g. W3110) or from bacteria derived from B strains (e.g. BL21). These strains are particularly useful because their growth parameters are extremely well known and robust. In addition, these strains are non-pathogenic, which is commercially important for safety and environmental reasons. Other examples of suitable *E. coli* hosts include, but are not limited to, strains of BL21, DH10B, or derivatives thereof. In another embodiment of the methods of the present invention, the *E. coli* host is a protease minus strain including, but not limited to, OMP- and LON-. The host cell strain may be a species of

Pseudomonas, including but not limited to, *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, and *Pseudomonas putida*, *Pseudomonas fluorescens* biovar 1, designated strain MB101, is known to be useful for recombinant production and is available for therapeutic protein production processes. Examples of a *Pseudomonas* expression system include the system available from The Dow Chemical Company as a host strain (Midland, Mich. available on the World Wide Web at dow.com).

Once a recombinant host cell strain has been established (i.e., the expression construct has been introduced into the host cell and host cells with the proper expression construct are isolated), the recombinant host cell strain is cultured under conditions appropriate for production of hPP or hA or hFc polypeptides. As will be apparent to one of skill in the art, the method of culture of the recombinant host cell strain will be dependent on the nature of the expression construct utilized and the identity of the host cell. Recombinant host strains are normally cultured using methods that are known to those of ordinary skill in the art. Recombinant host cells are typically cultured in liquid medium containing assimilable sources of carbon, nitrogen, and inorganic salts and, optionally, containing vitamins, amino acids, growth factors, and other proteinaceous culture supplements known to those of ordinary skill in the art. Liquid media for culture of host cells may optionally contain antibiotics or anti-fungals to prevent the growth of undesirable microorganisms and/or compounds including, but not limited to, antibiotics to select for host cells containing the expression vector.

Recombinant host cells may be cultured in batch or continuous formats, with either cell harvesting (in the case where the hPP or hA or hFc polypeptide accumulates intracellularly) or harvesting of culture supernatant in either batch or continuous formats. For production in prokaryotic host cells, batch culture and cell harvest are preferred.

The hPP or hA or hFc polypeptides of the present invention are normally purified after expression in recombinant systems. The hPP or hA or hFc polypeptide may be purified from host cells or culture medium by a variety of methods known to the art. hPP or hA or hFc polypeptides produced in bacterial host cells may be poorly soluble or insoluble (in the form of inclusion bodies). In one embodiment of the present inven-

tion, amino acid substitutions may readily be made in the hPP or hA or hFc polypeptide that are selected for the purpose of increasing the solubility of the recombinantly produced protein utilizing the methods disclosed herein as well as those known in the art. In the case of insoluble protein, the protein may be collected from host cell lysates by centrifugation and may further be followed by homogenization of the cells. In the case of poorly soluble protein, compounds including, but not limited to, polyethylene imine (PEI) may be added to induce the precipitation of partially soluble protein. The precipitated protein may then be conveniently collected by centrifugation. Recombinant host cells may be disrupted or homogenized to release the inclusion bodies from within the cells using a variety of methods known to those of ordinary skill in the art. Host cell disruption or homogenization may be performed using well known techniques including, but not limited to, enzymatic cell disruption, sonication, dounce homogenization, or high pressure release disruption. In one embodiment of the method of the present invention, the high pressure release technique is used to disrupt the *E. coli* host cells to release the inclusion bodies of the hPP or hA or hFc polypeptides. When handling inclusion bodies of hPP or hA or hFc polypeptide, it may be advantageous to minimize the homogenization time on repetitions in order to maximize the yield of inclusion bodies without loss due to factors such as solubilization, mechanical shearing or proteolysis.

Insoluble or precipitated hPP or hA or hFc polypeptide may then be solubilized using any of a number of suitable solubilization agents known to the art. The hPP or hA or hFc polypeptide may be solubilized with urea or guanidine hydrochloride. The volume of the solubilized hPP or hA or hFc polypeptide should be minimized so that large batches may be produced using conveniently manageable batch sizes. This factor may be significant in a large-scale commercial setting where the recombinant host may be grown in batches that are thousands of liters in volume. In addition, when manufacturing hPP or hA or hFc polypeptide in a large-scale commercial setting, in particular for human pharmaceutical uses, the avoidance of harsh chemicals that can damage the machinery and container, or the protein product itself, should be avoided, if possible. It has been shown in the method of the present invention that the milder denaturing agent urea can be used to solubilize the hPP or hA or hFc polypeptide inclusion bodies in place of the harsher denaturing agent guanidine hydrochloride. The use of urea significantly reduces the risk of damage to stainless steel equipment utilized in the manufacturing and purification process of hPP or hA or hFc polypeptide while efficiently solubilizing the hPP or hA or hFc polypeptide inclusion bodies.

In the case of soluble hPP or hA or hFc protein, the hPP or hA or hFc may be secreted into the periplasmic space or into the culture medium. In addition, soluble hPP or hA or hFc may be present in the cytoplasm of the host cells. It may be desired to concentrate soluble hPP or hA or hFc prior to performing purification steps. Standard techniques known to those of ordinary skill in the art may be used to concentrate soluble hPP or hA or hFc from, for example, cell lysates or culture medium. In addition, standard techniques known to those of ordinary skill in the art may be used to disrupt host cells and release soluble hPP or hA or hFc from the cytoplasm or periplasmic space of the host cells.

When hPP or hA or hFc polypeptide is produced as a fusion protein, the fusion sequence may be removed. Removal of a fusion sequence may be accomplished by enzymatic or chemical cleavage. Enzymatic removal of fusion sequences may be accomplished using methods known to those of ordinary skill in the art. The choice of enzyme for removal of the

fusion sequence will be determined by the identity of the fusion, and the reaction conditions will be specified by the choice of enzyme as will be apparent to one of ordinary skill in the art. Chemical cleavage may be accomplished using reagents known to those of ordinary skill in the art, including but not limited to, cyanogen bromide, TEV protease, and other reagents. The cleaved hPP or hA or hFc polypeptide may be purified from the cleaved fusion sequence by methods known to those of ordinary skill in the art. Such methods will be determined by the identity and properties of the fusion sequence and the hPP or hA or hFc polypeptide, as will be apparent to one of ordinary skill in the art. Methods for purification may include, but are not limited to, size-exclusion chromatography, hydrophobic interaction chromatography, ion-exchange chromatography or dialysis or any combination thereof.

The hPP or hA or hFc polypeptide may also be purified to remove DNA from the protein solution. DNA may be removed by any suitable method known to the art, such as precipitation or ion exchange chromatography, but may be removed by precipitation with a nucleic acid precipitating agent, such as, but not limited to, protamine sulfate. The hPP or hA or hFc polypeptide may be separated from the precipitated DNA using standard well known methods including, but not limited to, centrifugation or filtration. Removal of host nucleic acid molecules is an important factor in a setting where the hPP or hA or hFc polypeptide is to be used to treat humans and the methods of the present invention reduce host cell DNA to pharmaceutically acceptable levels.

Methods for small-scale or large-scale fermentation can also be used in protein expression, including but not limited to, fermentors, shake flasks, fluidized bed bioreactors, hollow fiber bioreactors, roller bottle culture systems, and stirred tank bioreactor systems. Each of these methods can be performed in a batch, fed-batch, or continuous mode process.

Human hPP or hA or hFc polypeptides of the invention can generally be recovered using methods standard in the art. For example, culture medium or cell lysate can be centrifuged or filtered to remove cellular debris. The supernatant may be concentrated or diluted to a desired volume or diafiltered into a suitable buffer to condition the preparation for further purification. Further purification of the hPP or hA or hFc polypeptide of the present invention includes separating deamidated and clipped forms of the hPP or hA or hFc polypeptide variant from the intact form.

Any of the following exemplary procedures can be employed for purification of hPP or hA polypeptides of the invention: affinity chromatography; anion- or cation-exchange chromatography (using, including but not limited to, DEAF SEPHAROSE); chromatography on silica; high performance liquid chromatography (HPLC); reverse phase HPLC; gel filtration (using, including but not limited to, SEPHADEX G-75); hydrophobic interaction chromatography; size-exclusion chromatography; metal-chelate chromatography; ultrafiltration/diafiltration; ethanol precipitation; ammonium sulfate precipitation; chromatofocusing; displacement chromatography; electrophoretic procedures (including but not limited to preparative isoelectric focusing), differential solubility (including but not limited to ammonium sulfate precipitation), SDS-PAGE, or extraction.

Proteins of the present invention, including but not limited to, proteins comprising unnatural amino acids, peptides comprising unnatural amino acids, antibodies to proteins comprising unnatural amino acids, binding partners for proteins comprising unnatural amino acids, etc., can be purified, either partially or substantially to homogeneity, according to standard procedures known to and used by those of skill in the art.

Accordingly, polypeptides of the invention can be recovered and purified by any of a number of methods known to those of ordinary skill in the art, including but not limited to, ammonium sulfate or ethanol precipitation, acid or base extraction, column chromatography, affinity column chromatography, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography, lectin chromatography, gel electrophoresis and the like. Protein refolding steps can be used, as desired, in making correctly folded mature proteins. High performance liquid chromatography (HPLC), affinity chromatography or other suitable methods can be employed in final purification steps where high purity is desired. In one embodiment, antibodies made against unnatural amino acids (or proteins or peptides comprising unnatural amino acids) are used as purification reagents, including but not limited to, for affinity-based purification of proteins or peptides comprising one or more unnatural amino acid(s). Once purified, partially or to homogeneity, as desired, the polypeptides are optionally used for a wide variety of utilities, including but not limited to, as assay components, therapeutics, prophylaxis, diagnostics, research reagents, and/or as immunogens for antibody production.

In addition to other references noted herein, a variety of purification/protein folding methods are known to those of ordinary skill in the art, including, but not limited to, those set forth in R. Scopes, *Protein Purification*, Springer-Verlag, N.Y. (1982); Deutscher, *Methods in Enzymology Vol. 182: Guide to Protein Purification*, Academic Press, Inc. N.Y. (1990); Sandana, (1997) *Bioseparation of Proteins*, Academic Press, Inc.; Bollag et al. (1996) *Protein Methods*, 2nd Edition Wiley-Liss, NY; Walker, (1996) *The Protein Protocols Handbook* Humana Press, NJ; Harris and Angal, (1990) *Protein Purification Applications: A Practical Approach* IRL Press at Oxford, Oxford, England; Harris and Angal, *Protein Purification Methods: A Practical Approach* IRL Press at Oxford, Oxford, England; Scopes, (1993) *Protein Purification: Principles and Practice 3rd Edition* Springer Verlag, NY; Janson and Ryden, (1998) *Protein Purification Principles, High Resolution Methods and Applications, Second Edition* Wiley-VCH, NY; and Walker (1998), *Protein Protocols on CD-ROM* Humana Press, NJ; and the references cited therein.

One advantage of producing a protein or polypeptide of interest with an unnatural amino acid in a eukaryotic host cell or non-eukaryotic host cell is that typically the proteins or polypeptides will be folded in their native conformations. However, in certain embodiments of the invention, those of skill in the art will recognize that, after synthesis, expression and/or purification, proteins or peptides can possess a conformation different from the desired conformations of the relevant polypeptides. In one aspect of the invention, the expressed protein or polypeptide is optionally denatured and then renatured. This is accomplished utilizing methods known in the art, including but not limited to, by adding a chaperonin to the protein or polypeptide of interest, by solubilizing the proteins in a chaotropic agent such as guanidine HCl, utilizing protein disulfide isomerase, etc.

In general, it is occasionally desirable to denature and reduce expressed polypeptides and then to cause the polypeptides to re-fold into the preferred conformation. For example, guanidine, urea, DTT, DTE, and/or a chaperonin can be added to a translation product of interest. Methods of reducing, denaturing and renaturing proteins are known to those of ordinary skill in the art (see, the references above, and Debin-ski, et al. (1993) *J. Biol. Chem.*, 268: 14065-14070; Kreitman and Pastan (1993) *Bioconjug. Chem.*, 4: 581-585; and Buch-

ner, et al., (1992) *Anal. Biochem.*, 205: 263-270). Debinski, et al., for example, describe the denaturation and reduction of inclusion body proteins in guanidine-DTE. The proteins can be refolded in a redox buffer containing, including but not limited to, oxidized glutathione and L-arginine. Refolding reagents can be flowed or otherwise moved into contact with the one or more polypeptide or other expression product, or vice-versa.

In the case of prokaryotic production of hPP or hA or hFc polypeptide, the hPP or hA or hFc polypeptide thus produced may be misfolded and thus lacks or has reduced biological activity. The bioactivity of the protein may be restored by "refolding". In general, misfolded hPP or hA polypeptide is refolded by solubilizing (where the hPP or hA or hFc polypeptide is also insoluble), unfolding and reducing the polypeptide chain using, for example, one or more chaotropic agents (e.g. urea and/or guanidine) and a reducing agent capable of reducing disulfide bonds (e.g. dithiothreitol, DTT or 2-mercaptoethanol, 2-ME). At a moderate concentration of chaotrope, an oxidizing agent is then added (e.g., oxygen, cystine or cystamine), which allows the reformation of disulfide bonds. hPP or hA or hFc polypeptide may be refolded using standard methods known in the art, such as those described in U.S. Pat. Nos. 4,511,502, 4,511,503, and 4,512,922, which are incorporated by reference herein. The hPP or hA or hFc polypeptide may also be cofolded with other proteins to form heterodimers or heteromultimers.

After refolding, the hPP or hA or hFc may be further purified. Purification of hPP or hA or hFc may be accomplished using a variety of techniques known to those of ordinary skill in the art, including hydrophobic interaction chromatography, size exclusion chromatography, ion exchange chromatography, reverse-phase high performance liquid chromatography, affinity chromatography, and the like or any combination thereof. Additional purification may also include a step of drying or precipitation of the purified protein.

After purification, hPP or hA or hFc may be exchanged into different buffers and/or concentrated by any of a variety of methods known to the art, including, but not limited to, diafiltration and dialysis. hPP or hA or hFc that is provided as a single purified protein may be subject to aggregation and precipitation.

The purified hPP or hA or hFc may be at least 90% pure (as measured by reverse phase high performance liquid chromatography, RP-HPLC, or sodium dodecyl sulfate-polyacrylamide gel electrophoresis, SDS-PAGE) or at least 95% pure, or at least 98% pure, or at least 99% or greater pure. Regardless of the exact numerical value of the purity of the hPP or hA or hFc, the hPP or hA or hFc is sufficiently pure for use as a pharmaceutical product or for further processing, such as conjugation with a water soluble polymer such as PEG.

Certain hPP or hA or hFc molecules may be used as therapeutic agents in the absence of other active ingredients or proteins (other than excipients, carriers, and stabilizers, serum albumin and the like), or they may be complexed with another protein or a polymer.

General Purification Methods Any one of a variety of isolation steps may be performed on the cell lysate, extract, culture medium, inclusion bodies, periplasmic space of the host cells, cytoplasm of the host cells, or other material, comprising hPP or hA or hFc polypeptide or on any hPP or hA or hFc polypeptide mixtures resulting from any isolation steps including, but not limited to, affinity chromatography, ion exchange chromatography, hydrophobic interaction chromatography, gel filtration chromatography, high performance liquid chromatography ("HPLC"), reversed phase-HPLC

("RP-HPLC"), expanded bed adsorption, or any combination and/or repetition thereof and in any appropriate order.

Equipment and other necessary materials used in performing the techniques described herein are commercially available. Pumps, fraction collectors, monitors, recorders, and entire systems are available from, for example, Applied Biosystems (Foster City, Calif.), Bio-Rad Laboratories, Inc. (Hercules, Calif.), and Amersham Biosciences, Inc. (Piscataway, N.J.). Chromatographic materials including, but not limited to, exchange matrix materials, media, and buffers are also available from such companies.

Equilibration, and other steps in the column chromatography processes described herein such as washing and elution, may be more rapidly accomplished using specialized equipment such as a pump. Commercially available pumps include, but are not limited to, HILOAD® Pump P-50, Peristaltic Pump P-1, Pump P-901, and Pump P-903 (Amersham Biosciences, Piscataway, N.J.).

Examples of fraction collectors include RediFrac Fraction Collector, FRAC-100 and FRAC-200 Fraction Collectors, and SUPERFRAC® Fraction Collector (Amersham Biosciences, Piscataway, N.J.). Mixers are also available to form pH and linear concentration gradients. Commercially available mixers include Gradient Mixer GM-1 and In-Line Mixers (Amersham Biosciences, Piscataway, N.J.).

The chromatographic process may be monitored using any commercially available monitor. Such monitors may be used to gather information like UV, pH, and conductivity. Examples of detectors include Monitor UV-1, UVICORD® S II, Monitor UV-M II, Monitor UV-900, Monitor UPC-900, Monitor pH/C-900, and Conductivity Monitor (Amersham Biosciences, Piscataway, N.J.). Indeed, entire systems are commercially available including the various AKTA® systems from Amersham Biosciences (Piscataway, N.J.).

In one embodiment of the present invention, for example, the hPP or hA or hFc polypeptide may be reduced and denatured by first denaturing the resultant purified hPP or hA or hFc polypeptide in urea, followed by dilution into TRIS buffer containing a reducing agent (such as DTT) at a suitable pH. In another embodiment, the hPP or hA or hFc polypeptide is denatured in urea in a concentration range of between about 2 M to about 9 M, followed by dilution in TRIS buffer at a pH in the range of about 5.0 to about 8.0. The refolding mixture of this embodiment may then be incubated. In one embodiment, the refolding mixture is incubated at room temperature for four to twenty-four hours. The reduced and denatured hPP or hA or hFc polypeptide mixture may then be further isolated or purified.

As stated herein, the pH of the first hPP or hA or hFc polypeptide mixture may be adjusted prior to performing any subsequent isolation steps. In addition, the first hPP or hA or hFc polypeptide mixture or any subsequent mixture thereof may be concentrated using techniques known in the art. Moreover, the elution buffer comprising the first hPP or hA or hFc polypeptide mixture or any subsequent mixture thereof may be exchanged for a buffer suitable for the next isolation step using techniques known to those of ordinary skill in the art.

Ion Exchange Chromatography In one embodiment, and as an optional, additional step, ion exchange chromatography may be performed on the first hPP or hA or hFc polypeptide mixture. See generally ION EXCHANGE CHROMATOGRAPHY: PRINCIPLES AND METHODS (Cat. No. 18-1114-21, Amersham Biosciences (Piscataway, N.J.)). Commercially available ion exchange columns include HITRAP®, HIPREP®, and HILOAD® Columns (Amersham Biosciences, Piscataway, N.J.). Such columns utilize strong anion exchangers such as

Q SEPHAROSE® Fast Flow, Q SEPHAROSE® High Performance, and Q SEPHAROSE® XL; strong cation exchangers such as SP SEPHAROSE® High Performance, SP SEPHAROSE® Fast Flow, and SP SEPHAROSE® XL; weak anion exchangers such as DEAE SEPHAROSE® Fast Flow; and weak cation exchangers such as CM SEPHAROSE® Fast Flow (Amersham Biosciences, Piscataway, N.J.). Anion or cation exchange column chromatography may be performed on the hPP or hA or hFc polypeptide at any stage of the purification process to isolate substantially purified hPP or hA or hFc polypeptide. The cation exchange chromatography step may be performed using any suitable cation exchange matrix. Useful cation exchange matrices include, but are not limited to, fibrous, porous, non-porous, microgranular, beaded, or cross-linked cation exchange matrix materials. Such cation exchange matrix materials include, but are not limited to, cellulose, agarose, dextran, polyacrylate, polyvinyl, polystyrene, silica, polyether, or composites of any of the foregoing.

The cation exchange matrix may be any suitable cation exchanger including strong and weak cation exchangers. Strong cation exchangers may remain ionized over a wide pH range and thus, may be capable of binding hPP or hA or hFc over a wide pH range. Weak cation exchangers, however, may lose ionization as a function of pH. For example, a weak cation exchanger may lose charge when the pH drops below about pH 4 or pH 5. Suitable strong cation exchangers include, but are not limited to, charged functional groups such as sulfopropyl (SP), methyl sulfonate (S), or sulfoethyl (SE). The cation exchange matrix may be a strong cation exchanger, preferably having an hPP or hA or hFc binding pH range of about 2.5 to about 6.0. Alternatively, the strong cation exchanger may have an hPP or hA or hFc binding pH range of about pH 2.5 to about pH 5.5. The cation exchange matrix may be a strong cation exchanger having an hPP or hA or hFc binding pH of about 3.0. Alternatively, the cation exchange matrix may be a strong cation exchanger, preferably having an hPP or hA or hFc binding pH range of about 6.0 to about 8.0. The cation exchange matrix may be a strong cation exchanger preferably having an hPP or hA or hFc binding pH range of about 8.0 to about 12.5. Alternatively, the strong cation exchanger may have an hPP or hA binding pH range of about pH 8.0 to about pH 12.0.

Prior to loading the hPP or hA or hFc, the cation exchange matrix may be equilibrated, for example, using several column volumes of a dilute, weak acid, e.g., four column volumes of 20 mM acetic acid, pH 3. Following equilibration, the hPP or hA or hFc may be added and the column may be washed one to several times, prior to elution of substantially purified hPP or hA or hFc, also using a weak acid solution such as a weak acetic acid or phosphoric acid solution. For example, approximately 2-4 column volumes of 20 mM acetic acid, pH 3, may be used to wash the column. Additional washes using, e.g., 2-4 column volumes of 0.05 M sodium acetate, pH 5.5, or 0.05 M sodium acetate mixed with 0.1 M sodium chloride, pH 5.5, may also be used. Alternatively, using methods known in the art, the cation exchange matrix may be equilibrated using several column volumes of a dilute, weak base.

Alternatively, substantially purified hPP or hA or hFc may be eluted by contacting the cation exchanger matrix with a buffer having a sufficiently low pH or ionic strength to displace the hPP or hA from the matrix. The pH of the elution buffer may range from about pH 2.5 to about pH 6.0. More specifically, the pH of the elution buffer may range from about pH 2.5 to about pH 5.5, about pH 2.5 to about pH 5.0. The elution buffer may have a pH of about 3.0. In addition, the

quantity of elution buffer may vary widely and will generally be in the range of about 2 to about 10 column volumes.

Following adsorption of the hPP or hA or hFc polypeptide to the cation exchanger matrix, substantially purified hPP or hA or hFc polypeptide may be eluted by contacting the matrix with a buffer having a sufficiently high pH or ionic strength to displace the hPP or hA or hFc polypeptide from the matrix. Suitable buffers for use in high pH elution of substantially purified hPP or hA or hFc polypeptide may include, but not limited to, citrate, phosphate, formate, acetate, HEPES, and MES buffers ranging in concentration from at least about 5 mM to at least about 100 mM.

Reverse-Phase Chromatography RP-HPLC may be performed to purify proteins following suitable protocols that are known to those of ordinary skill in the art. See, e.g., Pearson et al., *ANAL. BIOCHEM.* (1982) 124:217-230 (1982); Rivier et al., *J. CHROM.* (1983) 268:112-119; Kunitani et al., *J. CHROM.* (1986) 359:391-402. RP-HPLC may be performed on the hPP or hA polypeptide to isolate substantially purified hPP or hA or hFc polypeptide. In this regard, silica derivatized resins with alkyl functionalities with a wide variety of lengths, including, but not limited to, at least about C₃ to at least about C₃₀, at least about C₃ to at least about C₂₀, or at least about C₃ to at least about C₁₈, resins may be used. Alternatively, a polymeric resin may be used. For example, TosoHaas Amberchrome CG1000sd resin may be used, which is a styrene polymer resin. Cyano or polymeric resins with a wide variety of alkyl chain lengths may also be used. Furthermore, the RP-HPLC column may be washed with a solvent such as ethanol. The Source RP column is another example of a RP-HPLC column.

A suitable elution buffer containing an ion pairing agent and an organic modifier such as methanol, isopropanol, tetrahydrofuran, acetonitrile or ethanol, may be used to elute the hPP or hA or hFc polypeptide from the RP-HPLC column. The most commonly used ion pairing agents include, but are not limited to, acetic acid, formic acid, perchloric acid, phosphoric acid, trifluoroacetic acid, heptafluorobutyric acid, triethylamine, tetramethylammonium, tetrabutylammonium, and triethylammonium acetate. Elution may be performed using one or more gradients or isocratic conditions, with gradient conditions preferred to reduce the separation time and to decrease peak width. Another method involves the use of two gradients with different solvent concentration ranges. Examples of suitable elution buffers for use herein may include, but are not limited to, ammonium acetate and acetonitrile solutions.

Hydrophobic Interaction Chromatography Purification Techniques Hydrophobic interaction chromatography (HIC) may be performed on the hPP or hA polypeptide. See generally *HYDROPHOBIC INTERACTION CHROMATOGRAPHY HANDBOOK: PRINCIPLES AND METHODS* (Cat. No. 18-1020-90, Amersham Biosciences (Piscataway, N.J.) which is incorporated by reference herein. Suitable HIC matrices may include, but are not limited to, alkyl- or aryl-substituted matrices, such as butyl-, hexyl-, octyl- or phenyl-substituted matrices including agarose, cross-linked agarose, sepharose, cellulose, silica, dextran, polystyrene, poly(methacrylate) matrices, and mixed mode resins, including but not limited to, a polyethylenamine resin or a butyl- or phenyl-substituted poly(methacrylate) matrix. Commercially available sources for hydrophobic interaction column chromatography include, but are not limited to, HITRAP®, HEPREP®, and HILOAD® columns (Amersham Biosciences, Piscataway, N.J.).

Briefly, prior to loading, the HIC column may be equilibrated using standard buffers known to those of ordinary skill in the art, such as an acetic acid/sodium chloride solution or

HEPES containing ammonium sulfate. Ammonium sulfate may be used as the buffer for loading the HIC column. After loading the hPP or hA or hFc polypeptide, the column may then be washed using standard buffers and conditions to remove unwanted materials but retaining the hPP or hA or hFc polypeptide on the HIC column. The hPP or hA or hFc polypeptide may be eluted with about 3 to about 10 column volumes of a standard buffer, such as a HEPES buffer containing EDTA and lower ammonium sulfate concentration than the equilibrating buffer, or an acetic acid/sodium chloride buffer, among others. A decreasing linear salt gradient using, for example, a gradient of potassium phosphate, may also be used to elute the hPP or hA or hFc molecules. The eluant may then be concentrated, for example, by filtration such as diafiltration or ultrafiltration. Diafiltration may be utilized to remove the salt used to elute the hPP or hA or hFc polypeptide.

Other Purification Techniques Yet another isolation step using, for example, gel filtration (GEL FILTRATION: PRINCIPLES AND METHODS (Cat. No. 18-1022-18, Amersham Biosciences, Piscataway, N.J.) which is incorporated by reference herein, hydroxyapatite chromatography (suitable matrices include, but are not limited to, HA-Ultrogel, High Resolution (Calbiochem), CHT Ceramic Hydroxyapatite (BioRad), Bio-Gel HTP Hydroxyapatite (BioRad)), HPLC, expanded bed adsorption, ultrafiltration, diafiltration, lyophilization, and the like, may be performed on the first hPP or hA or hFc polypeptide mixture or any subsequent mixture thereof, to remove any excess salts and to replace the buffer with a suitable buffer for the next isolation step or even formulation of the final drug product.

The non-naturally encoded amino acid present in the hPP or hA or hFc molecule may also be utilized to provide separation from other cellular proteins that do not contain the non-naturally encoded amino acid. Since the non-naturally encoded amino acid may comprise unique chemical functional groups, the coupling of the unique functional group to another molecule may provide a substantial purification step. For example, the non-naturally encoded amino acid may be coupled to another molecule that facilitates separation from other proteins. Such molecules for coupling to the non-natural amino acid include, but are not limited to, PEG and other polymers, beads, and other solid substrates.

The yield of hPP or hA or hFc polypeptide, including substantially purified hPP or hA or hFc polypeptide, may be monitored at each step described herein using techniques known to those of ordinary skill in the art. Such techniques may also be used to assess the yield of substantially purified hPP or hA or hFc polypeptide following the last isolation step. For example, the yield of hPP or hA or hFc polypeptide may be monitored using any of several reverse phase high pressure liquid chromatography columns, having a variety of alkyl chain lengths such as cyano RP-HPLC, C₁₈RP-HPLC; as well as cation exchange HPLC and gel filtration HPLC.

In specific embodiments of the present invention, the yield of hPP or hA or hFc after each purification step may be at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.9%, or at least about 99.99%, of the hPP or hA or hFc in the starting material for each purification step.

Purity may be determined using standard techniques, such as SDS-PAGE, or by measuring hPP or hA or hFc polypeptide using Western blot and ELISA assays. For example, polyclonal antibodies may be generated against proteins isolated from negative control yeast fermentation and the cation exchange recovery. The antibodies may also be used to probe for the presence of contaminating host cell proteins.

RP-HPLC material Vydac C4 (Vydac) consists of silica gel particles, the surfaces of which carry C4-alkyl chains. The separation of hPP or hA or hFc polypeptide from the proteinaceous impurities is based on differences in the strength of hydrophobic interactions. Elution is performed with an acetonitrile gradient in diluted trifluoroacetic acid. Preparative HPLC is performed using a stainless steel column (filled with 2.8 to 3.2 liter of Vydac C4 silicagel). The Hydroxyapatite Ultrogel eluate is acidified by adding trifluoroacetic acid and loaded onto the Vydac C4 column. For washing and elution an acetonitrile gradient in diluted trifluoroacetic acid is used. Fractions are collected and immediately neutralized with phosphate buffer. The hPP or hA or hFc polypeptide fractions which are within the IPC limits are pooled.

DEAE Sepharose (Pharmacia) material consists of diethylaminoethyl (DEAE)-groups which are covalently bound to the surface of Sepharose beads. The binding of hPP or hA or hFc polypeptide to the DEAE groups is mediated by ionic interactions. Acetonitrile and trifluoroacetic acid pass through the column without being retained. After these substances have been washed off, trace impurities are removed by washing the column with acetate buffer at a low pH. Then the column is washed with neutral phosphate buffer and hPP or hA or hFc polypeptide is eluted with a buffer with increased ionic strength. The column is packed with DEAE Sepharose fast flow. The column volume is adjusted to assure an hPP or hA polypeptide load in the range of 3-10 mg hPP or hA or hFc polypeptide/ml gel. The column is washed with water and equilibration buffer (sodium/potassium phosphate). The pooled fractions of the HPLC eluate are loaded and the column is washed with equilibration buffer. Then the column is washed with washing buffer (sodium acetate buffer) followed by washing with equilibration buffer. Subsequently, hPP or hA or hFc polypeptide is eluted from the column with elution buffer (sodium chloride, sodium/potassium phosphate) and collected in a single fraction in accordance with the master elution profile. The eluate of the DEAE Sepharose column is adjusted to the specified conductivity. The resulting drug substance is sterile filtered into Teflon bottles and stored at -70° C.

Additional methods that may be employed include, but are not limited to, steps to remove endotoxins. Endotoxins are lipopoly-saccharides (LPSs) which are located on the outer membrane of Gram-negative host cells, such as, for example, *Escherichia coli*. Methods for reducing endotoxin levels are known to one of ordinary skill in the art and include, but are not limited to, purification techniques using silica supports, glass powder or hydroxyapatite, reverse-phase, affinity, size-exclusion, anion-exchange chromatography, hydrophobic interaction chromatography, a combination of these methods, and the like. Modifications or additional methods may be required to remove contaminants such as co-migrating proteins from the polypeptide of interest. Methods for measuring endotoxin levels are known to one of ordinary skill in the art and include, but are not limited to, *Limulus Amebocyte Lysate* (LAL) assays. The Endosafe™-PTS assay is a colorimetric, single tube system that utilizes cartridges preloaded with LAL reagent, chromogenic substrate, and control standard endotoxin along with a handheld spectrophotometer. Alter-

nate methods include, but are not limited to, a Kinetic LAL method that is turbidimetric and uses a 96 well format.

A wide variety of methods and procedures can be used to assess the yield and purity of an hPP or hA protein comprising one or more non-naturally encoded amino acids, including but not limited to, the Bradford assay, SDS-PAGE, silver stained SDS-PAGE, coomassie stained SDS-PAGE, mass spectrometry (including but not limited to, MALDI-TOF) and other methods for characterizing proteins known to one of ordinary skill in the art.

Additional methods include, but are not limited to: SDS-PAGE coupled with protein staining methods, immunoblotting, matrix assisted laser desorption/ionization-mass spectrometry (MALDI-MS), liquid chromatography/mass spectrometry, isoelectric focusing, analytical anion exchange, chromatofocusing, and circular dichroism.

VIII. Expression in Alternate Systems

Several strategies have been employed to introduce unnatural amino acids into proteins in non-recombinant host cells, mutagenized host cells, or in cell-free systems. These systems are also suitable for use in making the hPP or hA or hFc polypeptides of the present invention. Derivatization of amino acids with reactive side-chains such as Lys, Cys and Tyr resulted in the conversion of lysine to N²-acetyl-lysine. Chemical synthesis also provides a straightforward method to incorporate unnatural amino acids. With the recent development of enzymatic ligation and native chemical ligation of peptide fragments, it is possible to make larger proteins. See, e.g., P. E. Dawson and S. B. H. Kent, *Annu. Rev. Biochem.*, 69:923 (2000). Chemical peptide ligation and native chemical ligation are described in U.S. Pat. No. 6,184,344, U.S. Patent Publication No. 2004/0138412, U.S. Patent Publication No. 2003/0208046, WO 02/098902, and WO 03/042235, which are incorporated by reference herein. A general in vitro biosynthetic method in which a suppressor tRNA chemically acylated with the desired unnatural amino acid is added to an in vitro extract capable of supporting protein biosynthesis, has been used to site-specifically incorporate over 100 unnatural amino acids into a variety of proteins of virtually any size. See, e.g., V. W. Cornish, D. Mendel and P. G. Schultz, *Angew. Chem. Int. Ed. Engl.*, 1995, 34:621 (1995); C. J. Noren, S. J. Anthony-Cahill, M. C. Griffith, P. G. Schultz, *A general method for site-specific incorporation of unnatural amino acids into proteins*, *Science* 244:182-188 (1989); and, J. D. Bain, C. G. Glabe, T. A. Dix, A. R. Chamberlin, E. S. Dila, *Biosynthetic site-specific incorporation of a non-natural amino acid into a polypeptide*, *J. Am. Chem. Soc.* 111:8013-8014 (1989). A broad range of functional groups has been introduced into proteins for studies of protein stability, protein folding, enzyme mechanism, and signal transduction.

An in vivo method, termed selective pressure incorporation, was developed to exploit the promiscuity of wild-type synthetases. See, e.g., N. Budisa, C. Minks, S. Alefelder, W. Wenger, F. M. Dong, L. Moroder and R. Huber, *FASEB J.*, 13:41 (1999). An auxotrophic strain, in which the relevant metabolic pathway supplying the cell with a particular natural amino acid is switched off, is grown in minimal media containing limited concentrations of the natural amino acid, while transcription of the target gene is repressed. At the onset of a stationary growth phase, the natural amino acid is depleted and replaced with the unnatural amino acid analog. Induction of expression of the recombinant protein results in the accumulation of a protein containing the unnatural analog. For example, using this strategy, o, m and p-fluorophenylalanines have been incorporated into proteins, and exhibit two characteristic shoulders in the UV spectrum which can be

easily identified, see, e.g., C. Minks, R. Huber, L. Moroder and N. Budisa, *Anal. Biochem.*, 284:29 (2000); trifluoromethionine has been used to replace methionine in bacteriophage T4 lysozyme to study its interaction with chitooligosaccharide ligands by ¹⁹F NMR, see, e.g., H. Duewel, E. Daub, V. Robinson and J. F. Honek, *Biochemistry*, 36:3404 (1997); and trifluoroleucine has been incorporated in place of leucine, resulting in increased thermal and chemical stability of a leucine-zipper protein. See, e.g., Y. Tang, G. Ghirlanda, W. A. Petka, T. Nakajima, W. F. DeGrado and D. A. Tirrell, *Angew. Chem. Int. Ed. Engl.*, 40:1494 (2001). Moreover, selenomethionine and telluromethionine are incorporated into various recombinant proteins to facilitate the solution of phases in X-ray crystallography. See, e.g., W. A. Hendrickson, J. R. Horton and D. M. Lemaster, *EMBO J.*, 9:1665 (1990); J. O. Boles, K. Lewinski, M. Kunkle, J. D. Odom, B. Dunlap, L. Lebioda and M. Hatada, *Nat. Struct. Biol.*, 1:283 (1994); N. Budisa, B. Steipe, P. Demange, C. Eckerskorn, J. Kellermann and R. Huber, *Eur. J. Biochem.*, 230:788 (1995); and, N. Budisa, W. Kambrock, S. Steinbacher, A. Humm, L. Prade, T. Neufeld, L. Moroder and R. Huber, *J. Mol. Biol.*, 270:616 (1997). Methionine analogs with alkene or alkyne functionalities have also been incorporated efficiently, allowing for additional modification of proteins by chemical means. See, e.g., J. C. van Hest and D. A. Tirrell, *FEBS Lett.*, 428:68 (1998); J. C. van Hest, K. L. Kiick and D. A. Tirrell, *J. Am. Chem. Soc.*, 122:1282 (2000); and, K. L. Kiick and D. A. Tirrell, *Tetrahedron*, 56:9487 (2000); U.S. Pat. No. 6,586,207; U.S. Patent Publication 2002/0042097, which are incorporated by reference herein.

The success of this method depends on the recognition of the unnatural amino acid analogs by aminoacyl-tRNA synthetases, which, in general, require high selectivity to insure the fidelity of protein translation. One way to expand the scope of this method is to relax the substrate specificity of aminoacyl-tRNA synthetases, which has been achieved in a limited number of cases. For example, replacement of Ala²⁹⁴ by Gly in *Escherichia coli* phenylalanyl-tRNA synthetase (PheRS) increases the size of substrate binding pocket, and results in the acylation of tRNA^{Phe} by p-Cl-phenylalanine (p-Cl-Phe). See, M. Ibba, P. Kast and H. Hennecke, *Biochemistry*, 33:7107 (1994). An *Escherichia coli* strain harboring this mutant PheRS allows the incorporation of p-Cl-phenylalanine or p-Br-phenylalanine in place of phenylalanine. See, e.g., M. Ibba and H. Hennecke, *FEBS Lett.*, 364:272 (1995); and, N. Sharma, R. Furter, P. Kast and D. A. Tirrell, *FEBS Lett.*, 467:37 (2000). Similarly, a point mutation Phe130Ser near the amino acid binding site of *Escherichia coli* tyrosyl-tRNA synthetase was shown to allow azatyrine to be incorporated more efficiently than tyrosine. See, F. Hamano-Takaku, T. Iwama, S. Saito-Yano, K. Takaku, Y. Monden, M. Kitabatake, D. Soll and S. Nishimura, *J. Biol. Chem.*, 275:40324 (2000).

Another strategy to incorporate unnatural amino acids into proteins in vivo is to modify synthetases that have proofreading mechanisms. These synthetases cannot discriminate and therefore activate amino acids that are structurally similar to the cognate natural amino acids. This error is corrected at a separate site, which deacylates the mischarged amino acid from the tRNA to maintain the fidelity of protein translation. If the proofreading activity of the synthetase is disabled, structural analogs that are misactivated may escape the editing function and be incorporated. This approach has been demonstrated recently with the valyl-tRNA synthetase (ValRS). See, V. Doring, H. D. Mootz, L. A. Naugle, T. L. Hendrickson, V. de Crecy-Lagard, P. Schimmel and P. Marliere, *Science*, 292:501 (2001). ValRS can misaminoacylate

tRNA^{Val} with Cys, Thr, or aminobutyrate (Abu); these non-cognate amino acids are subsequently hydrolyzed by the editing domain. After random mutagenesis of the *Escherichia coli* chromosome, a mutant *Escherichia coli* strain was selected that has a mutation in the editing site of ValRS. This edit-defective ValRS incorrectly charges tRNA^{Val} with Cys. Because Abu sterically resembles Cys (—SH group of Cys is replaced with —CH₃ in Abu), the mutant ValRS also incorporates Abu into proteins when this mutant *Escherichia coli* strain is grown in the presence of Abu. Mass spectrometric analysis shows that about 24% of valines are replaced by Abu at each valine position in the native protein.

Solid-phase synthesis and semisynthetic methods have also allowed for the synthesis of a number of proteins containing novel amino acids. For example, see the following publications and references cited within, which are as follows: Crick, F. H. C., Barrett, L., Brenner, S., Watts-Tobin, R. *General nature of the genetic code for proteins*. *Nature*, 192: 1227-1232 (1961); Hofmann, K., Bohn, H. *Studies on polypeptides. XXXVI. The effect of pyrazole-imidazole replacements on the S-protein activating potency of an S-peptide fragment*, *J. Am. Chem. Soc.*, 88(24):5914-5919 (1966); Kaiser, E. T. *Synthetic approaches to biologically active peptides and proteins including enzymes*, *Acc Chem Res*, 22:47-54 (1989); Nakatsuka, T., Sasaki, T., Kaiser, E. T. *Peptide segment coupling catalyzed by the semisynthetic enzyme thio-subtilisin*, *J Am Chem Soc*, 109:3808-3810 (1987); Schnolzer, M., Kent, S B H. *Constructing proteins by dovetailing unprotected synthetic peptides: backbone-engineered HIV protease*, *Science*, 256(5054):221-225 (1992); Chaiken, I. M. *Semisynthetic peptides and proteins*, *CRC Crit Rev Biochem*, 11(3):255-301 (1981); Offord, R. E. *Protein engineering by chemical means?* *Protein Eng.*, 1(3):151-157 (1987); and, Jackson, D. Y., Burnier, J., Quan, C., Stanley, M., Tom, J., Wells, J. A. *A Designed Peptide Ligase for Total Synthesis of Ribonuclease A with Unnatural Catalytic Residues*, *Science*, 266(5183):243 (1994).

Chemical modification has been used to introduce a variety of unnatural side chains, including cofactors, spin labels and oligonucleotides into proteins in vitro. See, e.g., Corey, D. R., Schultz, P. G. *Generation of a hybrid sequence-specific single-stranded deoxyribonuclease*, *Science*, 238(4832): 1401-1403 (1987); Kaiser, E. T., Lawrence D. S., Rokita, S. E. *The chemical modification of enzymatic specificity*, *Annu Rev Biochem*, 54:565-595 (1985); Kaiser, E. T., Lawrence, D. S. *Chemical mutation of enzyme active sites*, *Science*, 226 (4674):505-511 (1984); Neet, K. E., Nanci A, Koshland, D. E. *Properties of thiol-subtilisin*, *J. Biol. Chem.*, 243(24):6392-6401 (1968); Polgar, L. et M. L. Bender. *A new enzyme containing a synthetically formed active site. Thiol-subtilisin*. *J. Am. Chem Soc*, 88:3153-3154 (1966); and, Pollack, S. J., Nakayama, G. Schultz, P. G. *Introduction of nucleophiles and spectroscopic probes into antibody combining sites*, *Science*, 242(4881):1038-1040 (1988).

Alternatively, biosynthetic methods that employ chemically modified aminoacyl-tRNAs have been used to incorporate several biophysical probes into proteins synthesized in vitro. See the following publications and references cited within: Brunner, J. *New Photolabeling and crosslinking methods*, *Annu. Rev Biochem*, 62:483-514 (1993); and, Krieg, U. C., Walter, P., Hohnson, A. E. *Photocrosslinking of the signal sequence of nascent preprolactin of the 54-kilodalton polypeptide of the signal recognition particle*, *Proc. Natl. Acad. Sci*, 83(22):8604-8608 (1986).

Previously, it has been shown that unnatural amino acids can be site-specifically incorporated into proteins in vitro by the addition of chemically aminoacylated suppressor tRNAs

to protein synthesis reactions programmed with a gene containing a desired amber nonsense mutation. Using these approaches, one can substitute a number of the common twenty amino acids with close structural homologues, e.g., fluorophenylalanine for phenylalanine, using strains auxotrophic for a particular amino acid. See, e.g., Noren, C. J., Anthony-Cahill, Griffith, M. C., Schultz, P. G. *A general method for site-specific incorporation of unnatural amino acids into proteins*, *Science*, 244: 182-188 (1989); M. W. Nowak, et al., *Science* 268:439-442 (1995); Bain, J. D., Glabe, C. G., Dix, T. A., Chamberlin, A. R., Diala, E. S. *Biosynthetic site-specific Incorporation of a non-natural amino acid into a polypeptide*, *J. Am. Chem Soc*, 111:8013-8014 (1989); N. Budisa et al., *FASEB J*. 13:41-51 (1999); Ellman, J. A., Mendel, D., Anthony-Cahill, S., Noren, C. J., Schultz, P. G. *Bio-synthetic method for introducing unnatural amino acids site-specifically into proteins*, *Methods in Enz.*, vol. 202, 301-336 (1992); and, Mendel, D., Cornish, V. W. & Schultz, P. G. *Site-Directed Mutagenesis with an Expanded Genetic Code*, *Annu Rev Biophys. Biomol Struct.* 24, 435-62 (1995).

For example, a suppressor tRNA was prepared that recognized the stop codon UAG and was chemically aminoacylated with an unnatural amino acid. Conventional site-directed mutagenesis was used to introduce the stop codon TAG, at the site of interest in the protein gene. See, e.g., Sayers, J. R., Schmidt, W. Eckstein, F. *5'-3' Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis*, *Nucleic Acids Res*, 16(3):791-802 (1988). When the acylated suppressor tRNA and the mutant gene were combined in an in vitro transcription/translation system, the unnatural amino acid was incorporated in response to the UAG codon which gave a protein containing that amino acid at the specified position. Experiments using [³H]-Phe and experiments with α -hydroxy acids demonstrated that only the desired amino acid is incorporated at the position specified by the UAG codon and that this amino acid is not incorporated at any other site in the protein. See, e.g., Noren, et al, supra; Kobayashi et al., (2003) *Nature Structural Biology* 10(6):425-432; and, Ellman, J. A., Mendel, D., Schultz, P. G. *Site-specific incorporation of novel backbone structures into proteins*, *Science*, 255(5041): 197-200 (1992).

A tRNA may be aminoacylated with a desired amino acid by any method or technique, including but not limited to, chemical or enzymatic aminoacylation.

Aminoacylation may be accomplished by aminoacyl tRNA synthetases or by other enzymatic molecules, including but not limited to, ribozymes. The term "ribozyme" is interchangeable with "catalytic RNA." Cech and coworkers (Cech, 1987, *Science*, 236:1532-1539; McCordle et al., 1987, *Concepts Biochem*. 64:221-226) demonstrated the presence of naturally occurring RNAs that can act as catalysts (ribozymes). However, although these natural RNA catalysts have only been shown to act on ribonucleic acid substrates for cleavage and splicing, the recent development of artificial evolution of ribozymes has expanded the repertoire of catalysis to various chemical reactions. Studies have identified RNA molecules that can catalyze aminoacyl-RNA bonds on their own (2')3'-termini (Illangakere et al., 1995 *Science* 267:643-647), and an RNA molecule which can transfer an amino acid from one RNA molecule to another (Lohse et al., 1996, *Nature* 381:442-444).

U.S. Patent Application Publication 2003/0228593, which is incorporated by reference herein, describes methods to construct ribozymes and their use in aminoacylation of tRNAs with naturally encoded and non-naturally encoded amino acids. Substrate-immobilized forms of enzymatic molecules that can aminoacylate tRNAs, including but not lim-

ited to, ribozymes, may enable efficient affinity purification of the aminoacylated products. Examples of suitable substrates include agarose, sepharose, and magnetic beads. The production and use of a substrate-immobilized form of ribozyme for aminoacylation is described in Chemistry and Biology 2003, 10:1077-1084 and U.S. Patent Application Publication 2003/0228593, which are incorporated by reference herein.

Chemical aminoacylation methods include, but are not limited to, those introduced by Hecht and coworkers (Hecht, S. M. *Acc. Chem. Res.* 1992, 25, 545; Heckler, T. G.; Roeser, J. R.; Xu, C.; Chang, P.; Hecht, S. M. *Biochemistry* 1988, 27, 7254; Hecht, S. M.; Alford, B. L.; Kuroda, Y.; Kitano, S. J. *Biol. Chem.* 1978, 253, 4517) and by Schultz, Chamberlin, Dougherty and others (Cornish, V. W.; Mendel, D.; Schultz, P. G. *Angew. Chem. Int. Ed. Engl.* 1995, 34, 621; Robertson, S. A.; Ellman, J. A.; Schultz, P. G. *J. Am. Chem. Soc.* 1991, 113, 2722; Noren, C. J.; Anthony-Cahill, S. J.; Griffith, M. C.; Schultz, P. G. *Science* 1989, 244, 182; Bain, J. D.; Glabe, C. G.; Dix, T. A.; Chamberlin, A. R. *J. Am. Chem. Soc.* 1989, 111, 8013; Bain, J. D. et al. *Nature* 1992, 356, 537; Gallivan, J. P.; Lester, H. A.; Dougherty, D. A. *Chem. Biol.* 1997, 4, 740; Turcatti, et al. *J. Biol. Chem.* 1996, 271, 19991; Nowak, M. W. et al. *Science*, 1995, 268, 439; Saks, M. E. et al. *J. Biol. Chem.* 1996, 271, 23169; Hohsaka, T. et al. *J. Am. Chem. Soc.* 1999, 121, 34), which are incorporated by reference herein, to avoid the use of synthetases in aminoacylation. Such methods or other chemical aminoacylation methods may be used to aminoacylate tRNA molecules.

Methods for generating catalytic RNA may involve generating separate pools of randomized ribozyme sequences, performing directed evolution on the pools, screening the pools for desirable aminoacylation activity, and selecting sequences of those ribozymes exhibiting desired aminoacylation activity.

Ribozymes can comprise motifs and/or regions that facilitate acylation activity, such as a GGU motif and a U-rich region. For example, it has been reported that U-rich regions can facilitate recognition of an amino acid substrate, and a GGU-motif can form base pairs with the 3' termini of a tRNA. In combination, the GGU and motif and U-rich region facilitate simultaneous recognition of both the amino acid and tRNA simultaneously, and thereby facilitate aminoacylation of the 3' terminus of the tRNA.

Ribozymes can be generated by in vitro selection using a partially randomized r24mini conjugated with tRNA^{Asn}_{CCCG}, followed by systematic engineering of a consensus sequence found in the active clones. An exemplary ribozyme obtained by this method is termed "Fx3 ribozyme" and is described in U.S. Pub. App. No. 2003/0228593, the contents of which is incorporated by reference herein, acts as a versatile catalyst for the synthesis of various aminoacyl-tRNAs charged with cognate non-natural amino acids.

Immobilization on a substrate may be used to enable efficient affinity purification of the aminoacylated tRNAs. Examples of suitable substrates include, but are not limited to, agarose, sepharose, and magnetic beads. Ribozymes can be immobilized on resins by taking advantage of the chemical structure of RNA, such as the 3'-cis-diol on the ribose of RNA can be oxidized with periodate to yield the corresponding dialdehyde to facilitate immobilization of the RNA on the resin. Various types of resins can be used including inexpensive hydrazide resins wherein reductive amination makes the interaction between the resin and the ribozyme an irreversible linkage. Synthesis of aminoacyl-tRNAs can be significantly

facilitated by this on-column aminoacylation technique. Kourouklis et al. *Methods* 2005; 36:239-4 describe a column-based aminoacylation system.

Isolation of the aminoacylated tRNAs can be accomplished in a variety of ways. One suitable method is to elute the aminoacylated tRNAs from a column with a buffer such as a sodium acetate solution with 10 mM EDTA, a buffer containing 50 mM N-(2-hydroxyethyl)piperazine-N'-(3-propanesulfonic acid), 12.5 mM KCl, pH 7.0, 10 mM EDTA, or simply an EDTA buffered water (pH 7.0).

The aminoacylated tRNAs can be added to translation reactions in order to incorporate the amino acid with which the tRNA was aminoacylated in a position of choice in a polypeptide made by the translation reaction. Examples of translation systems in which the aminoacylated tRNAs of the present invention may be used include, but are not limited to cell lysates. Cell lysates provide reaction components necessary for in vitro translation of a polypeptide from an input mRNA. Examples of such reaction components include but are not limited to ribosomal proteins, rRNA, amino acids, tRNAs, GTP, ATP, translation initiation and elongation factors and additional factors associated with translation. Additionally, translation systems may be batch translations or compartmentalized translation. Batch translation systems combine reaction components in a single compartment while compartmentalized translation systems separate the translation reaction components from reaction products that can inhibit the translation efficiency. Such translation systems are available commercially.

Further, a coupled transcription/translation system may be used. Coupled transcription/translation systems allow for both transcription of an input DNA into a corresponding mRNA, which is in turn translated by the reaction components. An example of a commercially available coupled transcription/translation is the Rapid Translation System (RTS, Roche Inc.). The system includes a mixture containing *E. coli* lysate for providing translational components such as ribosomes and translation factors. Additionally, an RNA polymerase is included for the transcription of the input DNA into an mRNA template for use in translation. RTS can use compartmentalization of the reaction components by way of a membrane interposed between reaction compartments, including a supply/waste compartment and a transcription/translation compartment.

Aminoacylation of tRNA may be performed by other agents, including but not limited to, transferases, polymerases, catalytic antibodies, multi-functional proteins, and the like.

Stephan in *Scientist* 2005 Oct 10; pages 30-33 describes additional methods to incorporate non-naturally encoded amino acids into proteins. Lu et al. in *Mol. Cell.* 2001 October; 8(4):759-69 describe a method in which a protein is chemically ligated to a synthetic peptide containing unnatural amino acids (expressed protein ligation).

Microinjection techniques have also been used to incorporate unnatural amino acids into proteins. See, e.g., M. W. Nowak, P. C. Kearney, J. R. Sampson, M. E. Saks, C. G. Labarca, S. K. Silverman, W. G. Zhong, J. Thorson, J. N. Abelson, N. Davidson, P. G. Schultz, D. A. Dougherty and H. A. Lester, *Science*, 268:439 (1995); and, D. A. Dougherty, *Curr. Opin. Chem. Biol.*, 4:645 (2000). A *Xenopus* oocyte was coinjected with two RNA species made in vitro: an mRNA encoding the target protein with a UAG stop codon at the amino acid position of interest and an amber suppressor tRNA aminoacylated with the desired unnatural amino acid. The translational machinery of the oocyte then inserts the unnatural amino acid at the position specified by UAG. This method has

allowed in vivo structure-function studies of integral membrane proteins, which are generally not amenable to in vitro expression systems. Examples include the incorporation of a fluorescent amino acid into tachykinin neurokinin-2 receptor to measure distances by fluorescence resonance energy transfer, see, e.g., G. Turcatti, K. Nemeth, M. D. Edgerton, U. Meseth, F. Talabot, M. Peitsch, J. Knowles, H. Vogel and A. Chollet, *J. Biol. Chem.*, 271:19991 (1996); the incorporation of biotinylated amino acids to identify surface-exposed residues in ion channels, see, e.g., J. P. Gallivan, H. A. Lester and D. A. Dougherty, *Chem. Biol.*, 4:739 (1997); the use of caged tyrosine analogs to monitor conformational changes in an ion channel in real time, see, e.g., J. C. Miller, S. K. Silverman, P. M. England, D. A. Dougherty and H. A. Lester, *Neuron*, 20:619 (1998); and, the use of alpha hydroxy amino acids to change ion channel backbones for probing their gating mechanisms. See, e.g., P. M. England, Y. Zhang, D. A. Dougherty and H. A. Lester, *Cell*, 96:89 (1999); and, T. Lu, A. Y. Ting, J. Mainland, L. Y. Jan, P. G. Schultz and J. Yang, *Nat. Neurosci.*, 4:239 (2001).

The ability to incorporate unnatural amino acids directly into proteins in vivo offers a wide variety of advantages including but not limited to, high yields of mutant proteins, technical ease, the potential to study the mutant proteins in cells or possibly in living organisms and the use of these mutant proteins in therapeutic treatments and diagnostic uses. The ability to include unnatural amino acids with various sizes, acidities, nucleophilicities, hydrophobicities, and other properties into proteins can greatly expand our ability to rationally and systematically manipulate the structures of proteins, both to probe protein function and create new proteins or organisms with novel properties.

In one attempt to site-specifically incorporate para-F-Phe, a yeast amber suppressor tRNA^{Phe}CUA/phenylalanyl-tRNA synthetase pair was used in a p-F-Phe resistant, Phe auxotrophic *Escherichia coli* strain. See, e.g., R. Furter, *Protein Sci.*, 7:419 (1998).

It may also be possible to obtain expression of an hPP or hA or hFc polynucleotide of the present invention using a cell-free (in-vitro) translational system. Translation systems may be cellular or cell-free, and may be prokaryotic or eukaryotic. Cellular translation systems include, but are not limited to, whole cell preparations such as permeabilized cells or cell cultures wherein a desired nucleic acid sequence can be transcribed to mRNA and the mRNA translated. Cell-free translation systems are commercially available and many different types and systems are well-known. Examples of cell-free systems include, but are not limited to, prokaryotic lysates such as *Escherichia coli* lysates, and eukaryotic lysates such as wheat germ extracts, insect cell lysates, rabbit reticulocyte lysates, rabbit oocyte lysates and human cell lysates. Eukaryotic extracts or lysates may be preferred when the resulting protein is glycosylated, phosphorylated or otherwise modified because many such modifications are only possible in eukaryotic systems. Some of these extracts and lysates are available commercially (Promega; Madison, Wis.; Stratagene; La Jolla, Calif.; Amersham; Arlington Heights, Ill.; GIBCO/BRL; Grand Island, N.Y.). Membranous extracts, such as the canine pancreatic extracts containing microsomal membranes, are also available which are useful for translating secretory proteins. In these systems, which can include either mRNA as a template (in-vitro translation) or DNA as a template (combined in-vitro transcription and translation), the in vitro synthesis is directed by the ribosomes. Considerable effort has been applied to the development of cell-free protein expression systems. See, e.g., Kim, D. M. and J. R. Swartz, *Biotechnology and Bioengineering*, 74 :309-316 (2001);

Kim, D. M. and J. R. Swartz, *Biotechnology Letters*, 22, 1537-1542, (2000); Kim, D. M., and J. R. Swartz, *Biotechnology Progress*, 16, 385-390, (2000); Kim, D. M., and J. R. Swartz, *Biotechnology and Bioengineering*, 66, 180-188, (1999); and Patnaik, R. and J. R. Swartz, *Biotechniques* 24, 862-868, (1998); U.S. Pat. No. 6,337,191; U.S. Patent Publication No. 2002/0081660; WO 00/55353; WO 90/05785, which are incorporated by reference herein. Another approach that may be applied to the expression of hPP or hA or hFc polypeptides comprising a non-naturally encoded amino acid includes the mRNA-peptide fusion technique. See, e.g., R. Roberts and J. Szostak, *Proc. Natl. Acad. Sci. (USA)* 94:12297-12302 (1997); A. Frankel, et al., *Chemistry & Biology* 10:1043-1050 (2003). In this approach, an mRNA template linked to puromycin is translated into peptide on the ribosome. If one or more tRNA molecules has been modified, non-natural amino acids can be incorporated into the peptide as well. After the last mRNA codon has been read, puromycin captures the C-terminus of the peptide. If the resulting mRNA-peptide conjugate is found to have interesting properties in an in vitro assay, its identity can be easily revealed from the mRNA sequence. In this way, one may screen libraries of hPP or hA or hFc polypeptides comprising one or more non-naturally encoded amino acids to identify polypeptides having desired properties. More recently, in vitro ribosome translations with purified components have been reported that permit the synthesis of peptides substituted with non-naturally encoded amino acids. See, e.g., A. Forster et al., *Proc. Natl. Acad. Sci. (USA)* 100:6353 (2003).

Reconstituted translation systems may also be used. Mixtures of purified translation factors have also been used successfully to translate mRNA into protein as well as combinations of lysates or lysates supplemented with purified translation factors such as initiation factor-1 (IF-1), IF-2, IF-3 (α or β), elongation factor T (EF-Tu), or termination factors. Cell-free systems may also be coupled transcription/translation systems wherein DNA is introduced to the system, transcribed into mRNA and the mRNA translated as described in *Current Protocols in Molecular Biology* (F. M. Ausubel et al. editors, Wiley Interscience, 1993), which is hereby specifically incorporated by reference. RNA transcribed in eukaryotic transcription system may be in the form of heteronuclear RNA (hnRNA) or 5'-end caps (7-methyl guanosine) and 3'-end poly A tailed mature mRNA, which can be an advantage in certain translation systems. For example, capped mRNAs are translated with high efficiency in the reticulocyte lysate system.

IX. Macromolecular Polymers Coupled to hPP or hA or hFc Polypeptides

Various modifications to the non-natural amino acid polypeptides described herein can be effected using the compositions, methods, techniques and strategies described herein. These modifications include the incorporation of further functionality onto the non-natural amino acid component of the polypeptide, including but not limited to, a label; a dye; a polymer; a water-soluble polymer; a derivative of polyethylene glycol; a photocrosslinker; a radionuclide; a cytotoxic compound; a drug; an affinity label; a photoaffinity label; a reactive compound; a resin; a second protein or polypeptide or polypeptide analog; an antibody or antibody fragment; a metal chelator; a cofactor; a fatty acid; a carbohydrate; a polynucleotide; a DNA; a RNA; an antisense polynucleotide; a saccharide; a water-soluble dendrimer; a cyclodextrin; an inhibitory ribonucleic acid; a biomaterial; a nanoparticle; a spin label; a fluorophore, a metal-containing moiety; a radioactive moiety; a novel functional group; a group that covalently or noncovalently interacts with other molecules; a

photocaged moiety; an actinic radiation excitable moiety; a photoisomerizable moiety; biotin; a derivative of biotin; a biotin analogue; a moiety incorporating a heavy atom; a chemically cleavable group; a photocleavable group; an elongated side chain; a carbon-linked sugar; a redox-active agent; an amino thioacid; a toxic moiety; an isotopically labeled moiety; a biophysical probe; a phosphorescent group; a chemiluminescent group; an electron dense group; a magnetic group; an intercalating group; a chromophore; an energy transfer agent; a biologically active agent; a detectable label; a small molecule; a quantum dot; a nanotransmitter; a radionucleotide; a radiotransmitter; a neutron-capture agent; or any combination of the above, or any other desirable compound or substance. As an illustrative, non-limiting example of the compositions, methods, techniques and strategies described herein, the following description will focus on adding macromolecular polymers to the non-natural amino acid polypeptide with the understanding that the compositions, methods, techniques and strategies described thereto are also applicable (with appropriate modifications, if necessary and for which one of skill in the art could make with the disclosures herein) to adding other functionalities, including but not limited to those listed above.

A wide variety of macromolecular polymers and other molecules can be linked to hPP or hA polypeptides of the present invention to modulate biological properties of the hPP or hA polypeptide, and/or provide new biological properties to the hPP or hA or hFc molecule. These macromolecular polymers can be linked to the hPP or hA or hFc polypeptide via a naturally encoded amino acid, via a non-naturally encoded amino acid, or any functional substituent of a natural or non-natural amino acid, or any substituent or functional group added to a natural or non-natural amino acid. The molecular weight of the polymer may be of a wide range, including but not limited to, between about 100 Da and about 100,000 Da or more. The molecular weight of the polymer may be between about 100 Da and about 100,000 Da, including but not limited to, 100,000 Da, 95,000 Da, 90,000 Da, 85,000 Da, 80,000 Da, 75,000 Da, 70,000 Da, 65,000 Da, 60,000 Da, 55,000 Da, 50,000 Da, 45,000 Da, 40,000 Da, 35,000 Da, 30,000 Da, 25,000 Da, 20,000 Da, 15,000 Da, 10,000 Da, 9,000 Da, 8,000 Da, 7,000 Da, 6,000 Da, 5,000 Da, 4,000 Da, 3,000 Da, 2,000 Da, 1,000 Da, 900 Da, 800 Da, 700 Da, 600 Da, 500 Da, 400 Da, 300 Da, 200 Da, and 100 Da. In some embodiments, the molecular weight of the polymer is between about 100 Da and 50,000 Da. In some embodiments, the molecular weight of the polymer is between about 100 Da and 40,000 Da. In some embodiments, the molecular weight of the polymer is between about 1,000 Da and 40,000 Da. In some embodiments, the molecular weight of the polymer is between about 5,000 Da and 40,000 Da. In some embodiments, the molecular weight of the polymer is between about 10,000 Da and 40,000 Da.

The present invention provides substantially homogenous preparations of polymer:protein conjugates. "Substantially homogenous" as used herein means that polymer:protein conjugate molecules are observed to be greater than half of the total protein. The polymer:protein conjugate has biological activity and the present "substantially homogenous" PEGylated hPP or hA or hFc polypeptide preparations provided herein are those which are homogenous enough to display the advantages of a homogenous preparation, e.g., ease in clinical application in predictability of lot to lot pharmacokinetics.

One may also choose to prepare a mixture of polymer:protein conjugate molecules, and the advantage provided herein is that one may select the proportion of mono-polymer:

protein conjugate to include in the mixture. Thus, if desired, one may prepare a mixture of various proteins with various numbers of polymer moieties attached (i.e., di-, tri-, tetra-, etc.) and combine said conjugates with the mono-polymer:protein conjugate prepared using the methods of the present invention, and have a mixture with a predetermined proportion of mono-polymer:protein conjugates.

The polymer selected may be water soluble so that the protein to which it is attached does not precipitate in an aqueous environment, such as a physiological environment. The polymer may be branched or unbranched. For therapeutic use of the end-product preparation, the polymer will be pharmaceutically acceptable.

Examples of polymers include but are not limited to polyalkyl ethers and alkoxy-capped analogs thereof (e.g., polyoxyethylene glycol, polyoxyethylene/propylene glycol, and methoxy or ethoxy-capped analogs thereof, especially polyoxyethylene glycol, the latter is also known as polyethyleneglycol or PEG); polyvinylpyrrolidones; polyvinylalkyl ethers; polyoxazolines, polyalkyl oxazolines and polyhydroxyalkyl oxazolines; polyacrylamides, polyalkyl acrylamides, and polyhydroxyalkyl acrylamides (e.g., polyhydroxypropylmethacrylamide and derivatives thereof); polyhydroxyalkyl acrylates; polysialic acids and analogs thereof; hydrophilic peptide sequences; polysaccharides and their derivatives, including dextran and dextran derivatives, e.g., carboxymethyl dextran, dextran sulfates, aminodextran; cellulose and its derivatives, e.g., carboxymethyl cellulose, hydroxyalkyl celluloses; chitin and its derivatives, e.g., chitosan, succinyl chitosan, carboxymethylchitin, carboxymethylchitosan; hyaluronic acid and its derivatives; starches; alginates; chondroitin sulfate; albumin; pullulan and carboxymethyl pullulan; polyaminoacids and derivatives thereof, e.g., polyglutamic acids, polylysines, polyaspartic acids, polyaspartamides; maleic anhydride copolymers such as: styrene maleic anhydride copolymer, divinylethyl ether maleic anhydride copolymer; polyvinyl alcohols; copolymers thereof; terpolymers thereof; mixtures thereof; and derivatives of the foregoing.

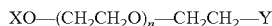
The proportion of polyethylene glycol molecules to protein molecules will vary, as will their concentrations in the reaction mixture. In general, the optimum ratio (in terms of efficiency of reaction in that there is minimal excess unreacted protein or polymer) may be determined by the molecular weight of the polyethylene glycol selected and on the number of available reactive groups available. As relates to molecular weight, typically the higher the molecular weight of the polymer, the fewer number of polymer molecules which may be attached to the protein. Similarly, branching of the polymer should be taken into account when optimizing these parameters. Generally, the higher the molecular weight (or the more branches) the higher the polymer:protein ratio.

As used herein, and when contemplating PEG:hPP or hA or hFc polypeptide conjugates, the term "therapeutically effective amount" refers to an amount which gives the desired benefit to a patient. The amount will vary from one individual to another and will depend upon a number of factors, including the overall physical condition of the patient and the underlying cause of the condition to be treated. The amount of hPP or hA or hFc polypeptide used for therapy gives an acceptable rate of change and maintains desired response at a beneficial level. A therapeutically effective amount of the present compositions may be readily ascertained by one of ordinary skill in the art using publicly available materials and procedures.

The water soluble polymer may be any structural form including but not limited to linear, forked or branched. Typically, the water soluble polymer is a poly(alkylene glycol),

such as polyethylene glycol) (PEG), but other water soluble polymers can also be employed. By way of example, PEG is used to describe certain embodiments of this invention.

PEG is a well-known, water soluble polymer that is commercially available or can be prepared by ring-opening polymerization of ethylene glycol according to methods known to those of ordinary skill in the art (Sandler and Karo, *Polymer Synthesis*, Academic Press, New York, Vol. 3, pages 138-161). The term "PEG" is used broadly to encompass any polyethylene glycol molecule, without regard to size or to modification at an end of the PEG, and can be represented as linked to the hPP or hA or hFc polypeptide by the formula:



where n is 2 to 10,000 and X is H or a terminal modification, including but not limited to, a C₁₋₄ alkyl, a protecting group, or a terminal functional group.

In some cases, a PEG used in the invention terminates on one end with hydroxy or methoxy, i.e., X is H or CH₃ ("methoxy PEG"). Alternatively, the PEG can terminate with a reactive group, thereby forming a bifunctional polymer. Typical reactive groups can include those reactive groups that are commonly used to react with the functional groups found in the 20 common amino acids (including but not limited to, maleimide groups, activated carbonates (including but not limited to, p-nitrophenyl ester), activated esters (including but not limited to, N-hydroxysuccinimide, p-nitrophenyl ester) and aldehydes) as well as functional groups that are inert to the 20 common amino acids but that react specifically with complementary functional groups present in non-naturally encoded amino acids (including but not limited to, azide groups, alkyne groups). It is noted that the other end of the PEG, which is shown in the above formula by Y, will attach either directly or indirectly to an hPP or hA or hFc polypeptide via a naturally-occurring or non-naturally encoded amino acid. For instance, Y may be an amide, carbamate or urea linkage to an amine group (including but not limited to, the epsilon amine of lysine or the N-terminus) of the polypeptide. Alternatively, Y may be a maleimide linkage to a thiol group (including but not limited to, the thiol group of cysteine). Alternatively, Y may be a linkage to a residue not commonly accessible via the 20 common amino acids. For example, an azide group on the PEG can be reacted with an alkyne group on the hPP or hA or hFc polypeptide to form a Huisgen [3+2] cycloaddition product. Alternatively, an alkyne group on the PEG can be reacted with an azide group present in a non-naturally encoded amino acid to form a similar product. In some embodiments, a strong nucleophile (including but not limited to, hydrazine, hydrazide, hydroxylamine, semicarbazide) can be reacted with an aldehyde or ketone group present in a non-naturally encoded amino acid to form a hydrazone, oxime or semicarbazone, as applicable, which in some cases can be further reduced by treatment with an appropriate reducing agent. Alternatively, the strong nucleophile can be incorporated into the hPP or hA or hFc polypeptide via a non-naturally encoded amino acid and used to react preferentially with a ketone or aldehyde group present in the water soluble polymer.

Any molecular mass for a PEG can be used as practically desired, including but not limited to, from about 100 Daltons (Da) to 100,000 Da or more as desired (including but not limited to, sometimes 0.1-50 kDa or 10-40 kDa). The molecular weight of PEG may be of a wide range, including but not limited to, between about 100 Da and about 100,000 Da or more. PEG may be between about 100 Da and about 100,000 Da, including but not limited to, 100,000 Da, 95,000 Da, 90,000 Da, 85,000 Da, 80,000 Da, 75,000 Da, 70,000 Da,

65,000 Da, 60,000 Da, 55,000 Da, 50,000 Da, 45,000 Da, 40,000 Da, 35,000 Da, 30,000 Da, 25,000 Da, 20,000 Da, 15,000 Da, 10,000 Da, 9,000 Da, 8,000 Da, 7,000 Da, 6,000 Da, 5,000 Da, 4,000 Da, 3,000 Da, 2,000 Da, 1,000 Da, 900 Da, 800 Da, 700 Da, 600 Da, 500 Da, 400 Da, 300 Da, 200 Da, and 100 Da. In some embodiments, PEG is between about 100 Da and 50,000 Da. In some embodiments, PEG is between about 100 Da and 40,000 Da. In some embodiments, PEG is between about 1,000 Da and 40,000 Da. In some embodiments, PEG is between about 5,000 Da and 40,000 Da. In some embodiments, PEG is between about 10,000 Da and 40,000 Da. Branched chain PEGs, including but not limited to, PEG molecules with each chain having a MW ranging from 1-100 kDa (including but not limited to, 1-50 kDa or 5-20 kDa) can also be used. The molecular weight of each chain of the branched chain PEG may be, including but not limited to, between about 1,000 Da and about 100,000 Da or more. The molecular weight of each chain of the branched chain PEG may be between about 1,000 Da and about 100,000 Da, including but not limited to, 100,000 Da, 95,000 Da, 90,000 Da, 85,000 Da, 80,000 Da, 75,000 Da, 70,000 Da, 65,000 Da, 60,000 Da, 55,000 Da, 50,000 Da, 45,000 Da, 40,000 Da, 35,000 Da, 30,000 Da, 25,000 Da, 20,000 Da, 15,000 Da, 10,000 Da, 9,000 Da, 8,000 Da, 7,000 Da, 6,000 Da, 5,000 Da, 4,000 Da, 3,000 Da, 2,000 Da, and 1,000 Da. In some embodiments, the molecular weight of each chain of the branched chain PEG is between about 1,000 Da and 50,000 Da. In some embodiments, the molecular weight of each chain of the branched chain PEG is between about 1,000 Da and 40,000 Da. In some embodiments, the molecular weight of each chain of the branched chain PEG is between about 5,000 Da and 40,000 Da. In some embodiments, the molecular weight of each chain of the branched chain PEG is between about 5,000 Da and 20,000 Da. A wide range of PEG molecules are described in, including but not limited to, the Shearwater Polymers, Inc. catalog, Nektar Therapeutics catalog, incorporated herein by reference.

Generally, at least one terminus of the PEG molecule is available for reaction with the non-naturally-encoded amino acid. For example, PEG derivatives bearing alkyne and azide moieties for reaction with amino acid side chains can be used to attach PEG to non-naturally encoded amino acids as described herein. If the non-naturally encoded amino acid comprises an azide, then the PEG will typically contain either an alkyne moiety to effect formation of the [3+2] cycloaddition product or an activated PEG species (i.e., ester, carbonate) containing a phosphine group to effect formation of the amide linkage. Alternatively, if the non-naturally encoded amino acid comprises an alkyne, then the PEG will typically contain an azide moiety to effect formation of the [3+2] Huisgen cycloaddition product. If the non-naturally encoded amino acid comprises a carbonyl group, the PEG will typically comprise a potent nucleophile (including but not limited to, a hydrazide, hydrazine, hydroxylamine, or semicarbazide functionality) in order to effect formation of corresponding hydrazone, oxime, and semicarbazone linkages, respectively. In other alternatives, a reverse of the orientation of the reactive groups described above can be used, i.e., an azide moiety in the non-naturally encoded amino acid can be reacted with a PEG derivative containing an alkyne.

In some embodiments, the hPP or hA or hFc polypeptide variant with a PEG derivative contains a chemical functionality that is reactive with the chemical functionality present on the side chain of the non-naturally encoded amino acid.

The invention provides in some embodiments azide- and acetylene-containing polymer derivatives comprising a water soluble polymer backbone having an average molecular

weight from about 800 Da to about 100,000 Da. The polymer backbone of the water-soluble polymer can be poly(ethylene glycol). However, it should be understood that a wide variety of water soluble polymers including but not limited to poly(ethylene)glycol and other related polymers, including poly(dextran) and poly(propylene glycol), are also suitable for use in the practice of this invention and that the use of the term PEG or poly(ethylene glycol) is intended to encompass and include all such molecules. The term PEG includes, but is not limited to, poly(ethylene glycol) in any of its forms, including bifunctional PEG, multiarmed PEG, derivatized PEG, forked PEG, branched PEG, pendent PEG (i.e. PEG or related polymers having one or more functional groups pendent to the polymer backbone), or PEG with degradable linkages therein.

PEG is typically clear, colorless, odorless, soluble in water, stable to heat, inert to many chemical agents, does not hydrolyze or deteriorate, and is generally non-toxic. Poly(ethylene glycol) is considered to be bio compatible, which is to say that PEG is capable of coexistence with living tissues or organisms without causing harm. More specifically, PEG is substantially non-immunogenic, which is to say that PEG does not tend to produce an immune response in the body. When attached to a molecule having some desirable function in the body, such as a biologically active agent, the PEG tends to mask the agent and can reduce or eliminate any immune response so that an organism can tolerate the presence of the agent. PEG conjugates tend not to produce a substantial immune response or cause clotting or other undesirable effects. PEG having the formula $-\text{CH}_2\text{CH}_2\text{O}-$ $(\text{CH}_2\text{CH}_2\text{O})_n-\text{CH}_2\text{CH}_2-$, where n is from about 3 to about 4000, typically from about 20 to about 2000, is suitable for use in the present invention. PEG having a molecular weight of from about 800 Da to about 100,000 Da are in some embodiments of the present invention particularly useful as the polymer backbone. The molecular weight of PEG may be of a wide range, including but not limited to, between about 100 Da and about 100,000 Da or more. The molecular weight of PEG may be between about 100 Da and about 100,000 Da, including but not limited to, 100,000 Da, 95,000 Da, 90,000 Da, 85,000 Da, 80,000 Da, 75,000 Da, 70,000 Da, 65,000 Da, 60,000 Da, 55,000 Da, 50,000 Da, 45,000 Da, 40,000 Da, 35,000 Da, 30,000 Da, 25,000 Da, 20,000 Da, 15,000 Da, 10,000 Da, 9,000 Da, 8,000 Da, 7,000 Da, 6,000 Da, 5,000 Da, 4,000 Da, 3,000 Da, 2,000 Da, 1,000 Da, 900 Da, 800 Da, 700 Da, 600 Da, 500 Da, 400 Da, 300 Da, 200 Da, and 100 Da. In some embodiments, the molecular weight of PEG is between about 100 Da and 50,000 Da. In some embodiments, the molecular weight of PEG is between about 100 Da and 40,000 Da. In some embodiments, the molecular weight of PEG is between about 1,000 Da and 40,000 Da. In some embodiments, the molecular weight of PEG is between about 5,000 Da and 40,000 Da. In some embodiments, the molecular weight of PEG is between about 10,000 Da and 40,000 Da.

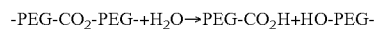
The polymer backbone can be linear or branched. Branched polymer backbones are generally known in the art. Typically, a branched polymer has a central branch core moiety and a plurality of linear polymer chains linked to the central branch core. PEG is commonly used in branched forms that can be prepared by addition of ethylene oxide to various polyols, such as glycerol, glycerol oligomers, pentaerythritol and sorbitol. The central branch moiety can also be derived from several amino acids, such as lysine. The branched poly(ethylene glycol) can be represented in general form as $\text{R}-(\text{PEG}-\text{OH})_m$ in which R is derived from a core moiety, such as glycerol, glycerol oligomers, or pentaerythritol, and m represents the number of arms. Multi-armed PEG

molecules, such as those described in U.S. Pat. Nos. 5,932,462; 5,643,575; 5,229,490; 4,289,872; U.S. Pat. Appl. 2003/0143596; WO 96/21469; and WO 93/21259, each of which is incorporated by reference herein in its entirety, can also be used as the polymer backbone.

Branched PEG can also be in the form of a forked PEG represented by $\text{PEG}(-\text{YCHZ}_2)_n$, where Y is a linking group and Z is an activated terminal group linked to CH by a chain of atoms of defined length.

Yet another branched form, the pendant PEG, has reactive groups, such as carboxyl, along the PEG backbone rather than at the end of PEG chains.

In addition to these forms of PEG, the polymer can also be prepared with weak or degradable linkages in the backbone. For example, PEG can be prepared with ester linkages in the polymer backbone that are subject to hydrolysis. As shown below, this hydrolysis results in cleavage of the polymer into fragments of lower molecular weight:



It is understood by those of ordinary skill in the art that the term poly(ethylene glycol) or PEG represents or includes all the forms known in the art including but not limited to those disclosed herein.

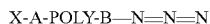
Many other polymers are also suitable for use in the present invention. In some embodiments, polymer backbones that are water-soluble, with from 2 to about 300 termini, are particularly useful in the invention. Examples of suitable polymers include, but are not limited to, other poly(alkylene glycols), such as polypropylene glycol ("PPG"), copolymers thereof (including but not limited to copolymers of ethylene glycol and propylene glycol), terpolymers thereof, mixtures thereof, and the like. Although the molecular weight of each chain of the polymer backbone can vary, it is typically in the range of from about 800 Da to about 100,000 Da, often from about 6,000 Da to about 80,000 Da. The molecular weight of each chain of the polymer backbone may be between about 100 Da and about 100,000 Da, including but not limited to, 100,000 Da, 95,000 Da, 90,000 Da, 85,000 Da, 80,000 Da, 75,000 Da, 70,000 Da, 65,000 Da, 60,000 Da, 55,000 Da, 50,000 Da, 45,000 Da, 40,000 Da, 35,000 Da, 30,000 Da, 25,000 Da, 20,000 Da, 15,000 Da, 10,000 Da, 9,000 Da, 8,000 Da, 7,000 Da, 6,000 Da, 5,000 Da, 4,000 Da, 3,000 Da, 2,000 Da, 1,000 Da, 900 Da, 800 Da, 700 Da, 600 Da, 500 Da, 400 Da, 300 Da, 200 Da, and 100 Da. In some embodiments, the molecular weight of each chain of the polymer backbone is between about 100 Da and 50,000 Da. In some embodiments, the molecular weight of each chain of the polymer backbone is between about 100 Da and 40,000 Da. In some embodiments, the molecular weight of each chain of the polymer backbone is between about 1,000 Da and 40,000 Da. In some embodiments, the molecular weight of each chain of the polymer backbone is between about 5,000 Da and 40,000 Da. In some embodiments, the molecular weight of each chain of the polymer backbone is between about 10,000 Da and 40,000 Da.

Those of ordinary skill in the art will recognize that the foregoing list for substantially water soluble backbones is by no means exhaustive and is merely illustrative, and that all polymeric materials having the qualities described above are contemplated as being suitable for use in the present invention.

In some embodiments of the present invention the polymer derivatives are "multi-functional", meaning that the polymer backbone has at least two termini, and possibly as many as about 300 termini, functionalized or activated with a functional group. Multifunctional polymer derivatives include,

but are not limited to, linear polymers having two termini, each terminus being bonded to a functional group which may be the same or different.

In one embodiment, the polymer derivative has the structure:



wherein:

N=N=N is an azide moiety;

B is a linking moiety, which may be present or absent;

POLY is a water-soluble non-antigenic polymer;

A is a linking moiety, which may be present or absent and which may be the same as B or different; and

X is a second functional group.

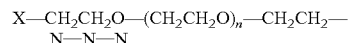
Examples of a linking moiety for A and B include, but are not limited to, a multiply-functionalized alkyl group containing up to 18, and may contain between 1-10 carbon atoms. A heteroatom such as nitrogen, oxygen or sulfur may be included with the alkyl chain. The alkyl chain may also be branched at a hetero atom. Other examples of a linking moiety for A and B include, but are not limited to, a multiply functionalized aryl group, containing up to 10 and may contain 5-6 carbon atoms. The aryl group may be substituted with one more carbon atoms, nitrogen, oxygen or sulfur atoms. Other examples of suitable linking groups include those linking groups described in U.S. Pat. Nos. 5,932,462; 5,643,575; and U.S. Pat. Appl. Publication 2003/0143596, each of which is incorporated by reference herein. Those of ordinary skill in the art will recognize that the foregoing list for linking moieties is by no means exhaustive and is merely illustrative, and that all linking moieties having the qualities described above are contemplated to be suitable for use in the present invention.

Examples of suitable functional groups for use as X include, but are not limited to, hydroxyl, protected hydroxyl, alkoxyl, active ester, such as N-hydroxysuccinimidyl esters and 1-benzotriazolyl esters, active carbonate, such as N-hydroxysuccinimidyl carbonates and 1-benzothiazolyl carbonates, acetal, aldehyde, aldehyde hydrates, alkenyl, acrylate, methacrylate, acrylamide, active sulfone, amine, aminoxy, protected amine, hydrazide, protected hydrazide, protected thiol, carboxylic acid, protected carboxylic acid, isocyanate, isothiocyanate, maleimide, vinylsulfone, dithiopyridine, vinylpyridine, iodoacetamide, epoxide, glyoxals, diones, mesylates, tosylates, tressylate, alkene, ketone, and azide. As is understood by those of ordinary skill in the art, the selected X moiety should be compatible with the azide group so that reaction with the azide group does not occur. The azide-containing polymer derivatives may be homobifunctional, meaning that the second functional group (i.e., X) is also an azide moiety, or heterobifunctional, meaning that the second functional group is a different functional group.

The term "protected" refers to the presence of a protecting group or moiety that prevents reaction of the chemically reactive functional group under certain reaction conditions. The protecting group will vary depending on the type of chemically reactive group being protected. For example, if the chemically reactive group is an amine or a hydrazide, the protecting group can be selected from the group of tert-butyloxycarbonyl (t-Boc) and 9-fluorenylmethoxycarbonyl (Fmoc). If the chemically reactive group is a thiol, the protecting group can be orthopyridyldisulfide. If the chemically reactive group is a carboxylic acid, such as butanoic or propionic acid, or a hydroxyl group, the protecting group can be benzyl or an alkyl group such as methyl, ethyl, or tert-butyl. Other protecting groups known in the art may also be used in the present invention.

Specific examples of terminal functional groups in the literature include, but are not limited to, N-succinimidyl carbonate (see e.g., U.S. Pat. Nos. 5,281,698, 5,468,478), amine (see, e.g., Buckmann et al. Makromol. Chem. 182:1379 (1981), Zalipsky et al. Eur. Polym. J. 19:1177 (1983)), hydrazide (see, e.g., Andresz et al. Makromol. Chem. 179:301 (1978)), succinimidyl propionate and succinimidyl butanoate (see, e.g., Olson et al. in Poly(ethylene glycol) Chemistry & Biological Applications, pp 170-181, Harris & Zalipsky Eds., ACS, Washington, D.C., 1997; see also U.S. Pat. No. 5,672,662), succinimidyl succinate (see, e.g., Abuchowski et al. Cancer Biochem. Biophys. 7:175 (1984) and Joppich et al. Makromol. Chem. 180:1381 (1979), succinimidyl ester (see, e.g., U.S. Pat. No. 4,670,417), benzotriazole carbonate (see, e.g., U.S. Pat. No. 5,650,234), glycidyl ether (see, e.g., Pitha et al. Eur. J. Biochem. 94:11 (1979), Elling et al., Biotech. Appl. Biochem. 13:354 (1991), oxycarbonylimidazole (see, e.g., Beauchamp, et al., Anal. Biochem. 131:25 (1983), Tondelli et al. J. Controlled Release 1:251 (1985)), p-nitrophenyl carbonate (see, e.g., Veronese, et al., Appl. Biochem. Biotech., 11: 141 (1985); and Sartore et al., Appl. Biochem. Biotech., 27:45 (1991)), aldehyde (see, e.g., Harris et al. J. Polym. Sci. Chem. Ed. 22:341 (1984), U.S. Pat. Nos. 5,824,784, 5,252,714), maleimide (see, e.g., Goodson et al. Biotechnology (NY) 8:343 (1990), Romani et al. in Chemistry of Peptides and Proteins 2:29 (1984)), and Kogan, Synthetic Comm. 22:2417 (1992)), orthopyridyl-disulfide (see, e.g., Woghiren, et al. Bioconj. Chem. 4:314 (1993)), acryloyl (see, e.g., Sawhney et al., Macromolecules, 26:581 (1993)), vinylsulfone (see, e.g., U.S. Pat. No. 5,900,461). All of the above references and patents are incorporated herein by reference.

In certain embodiments of the present invention, the polymer derivatives of the invention comprise a polymer backbone having the structure:

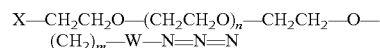


wherein:

X is a functional group as described above; and

n is about 20 to about 4000.

In another embodiment, the polymer derivatives of the invention comprise a polymer backbone having the structure:



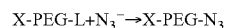
wherein:

W is an aliphatic or aromatic linker moiety comprising between 1-10 carbon atoms;

n is about 20 to about 4000; and

X is a functional group as described above. m is between 1 and 10.

The azide-containing PEG derivatives of the invention can be prepared by a variety of methods known in the art and/or disclosed herein. In one method, shown below, a water soluble polymer backbone having an average molecular weight from about 800 Da to about 100,000 Da, the polymer backbone having a first terminus bonded to a first functional group and a second terminus bonded to a suitable leaving group, is reacted with an azide anion (which may be paired with any of a number of suitable counter-ions, including sodium, potassium, tert-butylammonium and so forth). The leaving group undergoes a nucleophilic displacement and is replaced by the azide moiety, affording the desired azide-containing PEG polymer.

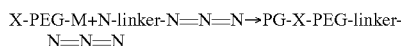


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As shown, a suitable polymer backbone for use in the present invention has the formula X-PEG-L, wherein PEG is poly(ethylene glycol) and X is a functional group which does not react with azide groups and L is a suitable leaving group. Examples of suitable functional groups include, but are not limited to, hydroxyl, protected hydroxyl, acetal, alkenyl, amine, minooxy, protected amine, protected hydrazide, protected thiol, carboxylic acid, protected carboxylic acid, maleimide, dithiopyridine, and vinylpyridine, and ketone. Examples of suitable leaving groups include, but are not limited to, chloride, bromide, iodide, mesylate, tresylate, and tosylate.

In another method for preparation of the azide-containing polymer derivatives of the present invention, a linking agent bearing an azide functionality is contacted with a water soluble polymer backbone having an average molecular weight from about 800 Da to about 100,000 Da, wherein the linking agent bears a chemical functionality that will react selectively with a chemical functionality on the PEG polymer, to form an azide-containing polymer derivative product wherein the azide is separated from the polymer backbone by a linking group.

An exemplary reaction scheme is shown below:



wherein:

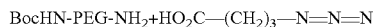
PEG is poly(ethylene glycol) and X is a capping group such as alkoxy or a functional group as described above; and

M is a functional group that is not reactive with the azide functionality but that will react efficiently and selectively with the N functional group.

Examples of suitable functional groups include, but are not limited to, M being a carboxylic acid, carbonate or active ester if N is an amine; M being a ketone if N is a hydrazide or aminooxy moiety; M being a leaving group if N is a nucleophile.

Purification of the crude product may be accomplished by known methods including, but are not limited to, precipitation of the product followed by chromatography, if necessary.

A more specific example is shown below in the case of PEG diamine, in which one of the amines is protected by a protecting group moiety such as tea-butyl-Boc and the resulting mono-protected PEG diamine is reacted with a linking moiety that bears the azide functionality:



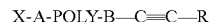
In this instance, the amine group can be coupled to the carboxylic acid group using a variety of activating agents such as thionyl chloride or carbodiimide reagents and N-hydroxysuccinimide or N-hydroxybenzotriazole to create an amide bond between the monoamine PEG derivative and the azide-bearing linker moiety. After successful formation of the amide bond, the resulting N-tert-butyl-Boc-protected azide-containing derivative can be used directly to modify bioactive molecules or it can be further elaborated to install other useful functional groups. For instance, the N-t-Boc group can be hydrolyzed by treatment with strong acid to generate an omega-amino-PEG-azide. The resulting amine can be used as a synthetic handle to install other useful functionality such as maleimide groups, activated disulfides, activated esters and so forth for the creation of valuable heterobifunctional reagents.

Heterobifunctional derivatives are particularly useful when it is desired to attach different molecules to each terminus of the polymer. For example, the omega-N-amino-N-azido PEG would allow the attachment of a molecule having

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an activated electrophilic group, such as an aldehyde, ketone, activated ester, activated carbonate and so forth, to one terminus of the PEG and a molecule having an acetylene group to the other terminus of the PEG.

In another embodiment of the invention, the polymer derivative has the structure:



wherein:

R can be either H or an alkyl, alkene, alkoxy, or aryl or substituted aryl group;

B is a linking moiety, which may be present or absent; POLY is a water-soluble non-antigenic polymer;

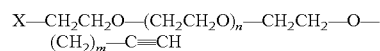
A is a linking moiety, which may be present or absent and which may be the same as B or different; and

X is a second functional group.

Examples of a linking moiety for A and B include, but are not limited to, a multiply-functionalized alkyl group containing up to 18, and may contain between 1-10 carbon atoms. A heteroatom such as nitrogen, oxygen or sulfur may be included with the alkyl chain. The alkyl chain may also be branched at a heteroatom. Other examples of a linking moiety for A and B include, but are not limited to, a multiply functionalized aryl group, containing up to 10 and may contain 5-6 carbon atoms. The aryl group may be substituted with one more carbon atoms, nitrogen, oxygen, or sulfur atoms. Other examples of suitable linking groups include those linking groups described in U.S. Pat. Nos. 5,932,462 and 5,643,575 and U.S. Pat. Appl. Publication 2003/0143596, each of which is incorporated by reference herein. Those of ordinary skill in the art will recognize that the foregoing list for linking moieties is by no means exhaustive and is intended to be merely illustrative, and that a wide variety of linking moieties having the qualities described above are contemplated to be useful in the present invention.

Examples of suitable functional groups for use as X include hydroxyl, protected hydroxyl, alkoxy, active ester, such as N-hydroxysuccinimidyl esters and 1-benzotriazolyl esters, active carbonate, such as N-hydroxysuccinimidyl carbonates and 1-benzotriazolyl carbonates, acetal, aldehyde, aldehyde hydrates, alkenyl, acrylate, methacrylate, acrylamide, active sulfone, amine, aminooxy, protected amine, hydrazide, protected hydrazide, protected thiol, carboxylic acid, protected carboxylic acid, isocyanate, isothiocyanate, maleimide, vinylsulfone, dithiopyridine, vinylpyridine, iodoacetamide, epoxide, glyoxals, diones, mesylates, tosylates, and tresylate, alkene, ketone, and acetylene. As would be understood, the selected X moiety should be compatible with the acetylene group so that reaction with the acetylene group does not occur. The acetylene-containing polymer derivatives may be homobifunctional, meaning that the second functional group (i.e., X) is also an acetylene moiety, or heterobifunctional, meaning that the second functional group is a different functional group.

In another embodiment of the present invention, the polymer derivatives comprise a polymer backbone having the structure:



wherein:

X is a functional group as described above;

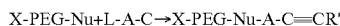
n is about 20 to about 4000; and

m is between 1 and 10.

Specific examples of each of the heterobifunctional PEG polymers are shown below.

The acetylene-containing PEG derivatives of the invention can be prepared using methods known to those of ordinary

skill in the art and/or disclosed herein. In one method, a water soluble polymer backbone having an average molecular weight from about 800 Da to about 100,000 Da, the polymer backbone having a first terminus bonded to a first functional group and a second terminus bonded to a suitable nucleophilic group, is reacted with a compound that bears both an acetylene functionality and a leaving group that is suitable for reaction with the nucleophilic group on the PEG. When the PEG polymer bearing the nucleophilic moiety and the molecule bearing the leaving group are combined, the leaving group undergoes a nucleophilic displacement and is replaced by the nucleophilic moiety, affording the desired acetylene-containing polymer.



As shown, a preferred polymer backbone for use in the reaction has the formula X-PEG-Nu, wherein PEG is poly(ethylene glycol), Nu is a nucleophilic moiety and X is a functional group that does not react with Nu, L or the acetylene functionality.

Examples of Nu include, but are not limited to, amine, alkoxy, aryloxy, sulfhydryl, imino, carboxylate, hydrazide, aminoxy groups that would react primarily via a SN2-type mechanism. Additional examples of Nu groups include those functional groups that would react primarily via a nucleophilic addition reaction. Examples of L groups include chloride, bromide, iodide, mesylate, tresylate, and tosylate and other groups expected to undergo nucleophilic displacement as well as ketones, aldehydes, thioesters, olefins, alpha-beta unsaturated carbonyl groups, carbonates and other electrophilic groups expected to undergo addition by nucleophiles.

In another embodiment of the present invention, A is an aliphatic linker of between 1-10 carbon atoms or a substituted aryl ring of between 6-14 carbon atoms. X is a functional group which does not react with azide groups and L is a suitable leaving group

In another method for preparation of the acetylene-containing polymer derivatives of the invention, a PEG polymer having an average molecular weight from about 800 Da to about 100,000 Da, bearing either a protected functional group or a capping agent at one terminus and a suitable leaving group at the other terminus is contacted by an acetylene anion.

An exemplary reaction scheme is shown below:



wherein:

PEG is poly(ethylene glycol) and X is a capping group such as alkoxy or a functional group as described above; and R' is either H, an alkyl, alkoxy, aryl or aryloxy group or a substituted alkyl, alkoxyl, aryl or aryloxy group.

In the example above, the leaving group L should be sufficiently reactive to undergo SN2-type displacement when contacted with a sufficient concentration of the acetylene anion. The reaction conditions required to accomplish SN2 displacement of leaving groups by acetylene anions are known to those of ordinary skill in the art.

Purification of the crude product can usually be accomplished by methods known in the art including, but are not limited to, precipitation of the product followed by chromatography, if necessary.

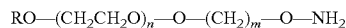
Water soluble polymers can be linked to the hPP or hA or hFc polypeptides of the invention. The water soluble polymers may be linked via a non-naturally encoded amino acid incorporated in the hPP or hA or hFc polypeptide or any functional group or substituent of a non-naturally encoded or naturally encoded amino acid, or any functional group or

substituent added to a non-naturally encoded or naturally encoded amino acid. Alternatively, the water soluble polymers are linked to an hPP or hA or hFc polypeptide incorporating a non-naturally encoded amino acid via a naturally-occurring amino acid (including but not limited to, cysteine, lysine or the amine group of the N-terminal residue). In some cases, the hPP or hA or hFc polypeptides of the invention comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 non-natural amino acids, wherein one or more non-naturally-encoded amino acid(s) are linked to water soluble polymer(s) (including but not limited to, PEG and/or oligosaccharides). In some cases, the hPP or hA or hFc polypeptides of the invention further comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more naturally-encoded amino acid(s) linked to water soluble polymers. In some cases, the hPP or hA or hFc polypeptides of the invention comprise one or more non-naturally encoded amino acid(s) linked to water soluble polymers and one or more naturally-occurring amino acids linked to water soluble polymers. In some embodiments, the water soluble polymers used in the present invention enhance the serum half-life of the hPP or hA or hFc polypeptide relative to the unconjugated form.

The number of water soluble polymers linked to an hPP or hA or hFc polypeptide (i.e., the extent of PEGylation or glycosylation) of the present invention can be adjusted to provide an altered (including but not limited to, increased or decreased) pharmacologic, pharmacokinetic or pharmacodynamic characteristic such as in vivo half-life. In some embodiments, the half-life of hPP or hA or hFc is increased at least about 10, 20, 30, 40, 50, 60, 70, 80, 90 percent, 2-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 11-fold, 12-fold, 13-fold, 14-fold, 15-fold, 16-fold, 17-fold, 18-fold, 19-fold, 20-fold, 25-fold, 30-fold, 35-fold, 40-fold, 50-fold, or at least about 100-fold over an unmodified polypeptide. PEG Derivatives Containing a Strong Nucleophilic Group (i.e., Hydrazide, Hydrazine, Hydroxylamine or Semicarbazide)

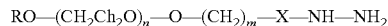
In one embodiment of the present invention, an hPP or hA or hFc polypeptide comprising a carbonyl-containing non-naturally encoded amino acid is modified with a PEG derivative that contains a terminal hydrazine, hydroxylamine, hydrazide or semicarbazide moiety that is linked directly to the PEG backbone.

In some embodiments, the hydroxylamine-terminal PEG derivative will have the structure:



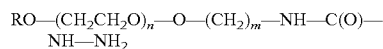
where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000 (i.e., average molecular weight is between 5-40 kDa).

In some embodiments, the hydrazine- or hydrazide-containing PEG derivative will have the structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000 and X is optionally a carbonyl group (C=O) that can be present or absent.

In some embodiments, the semicarbazide-containing PEG derivative will have the structure:

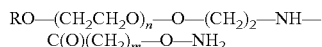


where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000.

In another embodiment of the invention, an hPP or hA or hFc polypeptide comprising a carbonyl-containing amino acid is modified with a PEG derivative that contains a termi-

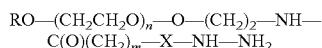
nal hydroxylamine, hydrazide, hydrazine, or semicarbazide moiety that is linked to the PEG backbone by means of an amide linkage.

In some embodiments, the hydroxylamine-terminal PEG derivatives have the structure:



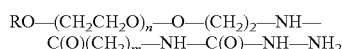
where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000 (i.e., average molecular weight is between 5-40 kDa).

In some embodiments, the hydrazine- or hydrazide-containing PEG derivatives have the structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10, n is 100-1,000 and X is optionally a carbonyl group (C=O) that can be present or absent.

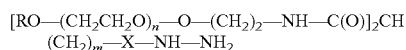
In some embodiments, the semicarbazide-containing PEG derivatives have the structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000.

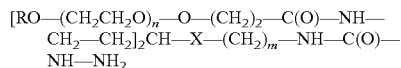
In another embodiment of the invention, an hPP or hA or hFc polypeptide comprising a carbonyl-containing amino acid is modified with a branched PEG derivative that contains a terminal hydrazine, hydroxylamine, hydrazide or semicarbazide moiety, with each chain of the branched PEG having a MW ranging from 10-40 kDa and, may be from 5-20 kDa.

In another embodiment of the invention, an hPP or hA or hFc polypeptide comprising a non-naturally encoded amino acid is modified with a PEG derivative having a branched structure. For instance, in some embodiments, the hydrazine- or hydrazide-terminal PEG derivative will have the following structure:



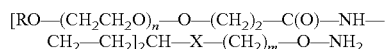
where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000, and X is optionally a carbonyl group (C=O) that can be present or absent.

In some embodiments, the PEG derivatives containing a semicarbazide group will have the structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), X is optionally NH, O, S, C(O) or not present, m is 2-10 and n is 100-1,000.

In some embodiments, the PEG derivatives containing a hydroxylamine group will have the structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), X is optionally NH, O, S, C(O) or not present, m is 2-10 and n is 100-1,000.

The degree and sites at which the water soluble polymer(s) are linked to the hPP or hA polypeptide can modulate the binding of the hPP or hA or hFc polypeptide to the hPP or hA or hFc polypeptide receptor or binding partner. In some embodiments, the linkages are arranged such that the hPP or hA or hFc polypeptide binds the hPP or hA polypeptide receptor or binding partner with a K_d of about 400 nM or lower, with a K_d of 150 nM or lower, and in some cases with

a K_d of 100 nM or lower, as measured by an equilibrium binding assay, such as that described in Spencer et al., *J. Biol. Chem.*, 263:7862-7867 (1988).

Methods and chemistry for activation of polymers as well as for conjugation of peptides are described in the literature and are known in the art. Commonly used methods for activation of polymers include, but are not limited to, activation of functional groups with cyanogen bromide, periodate, glutaraldehyde, biepoxydes, epichlorohydrin, divinylsulfone, carbodiimide, sulfonyl halides, trichlorotriazine, etc. (see, R. F. Taylor, (1991), *PROTEIN IMMOBILISATION. FUNDAMENTAL AND APPLICATIONS*, Marcel Dekker, N.Y.; S. S. Wong, (1992), *CHEMISTRY OF PROTEIN CONJUGATION AND CROSSLINKING*, CRC Press, Boca Raton; G. T. Hermanson et al., (1993), *IMMOBILIZED AFFINITY LIGAND TECHNIQUES*, Academic Press, N.Y.; Dunn, R. L., et al., Eds. *POLYMERIC DRUGS AND DRUG DELIVERY SYSTEMS*, ACS Symposium Series Vol. 469, American Chemical Society, Washington, D.C. 1991).

Several reviews and monographs on the functionalization and conjugation of PEG are available. See, for example, Harris, *Macromol. Chem. Phys. C25*: 325-373 (1985); Scouten, *Methods in Enzymology* 135: 30-65 (1987); Wong et al., *Enzyme Microb. Technol.* 14: 866-874 (1992); Delgado et al., *Critical Reviews in Therapeutic Drug Carrier Systems* 9: 249-304 (1992); Zalipsky, *Bioconjugate Chem.* 6: 150-165 (1995).

Methods for activation of polymers can also be found in WO 94/17039, U.S. Pat. No. 5,324,844, WO 94/18247, WO 94/04193, U.S. Pat. Nos. 5,219,564, 5,122,614, WO 90/13540, U.S. Pat. No. 5,281,698, and WO 93/15189, and for conjugation between activated polymers and enzymes including but not limited to Coagulation Factor VIII (WO 94/15625), hemoglobin (WO 94/09027), oxygen carrying molecule (U.S. Pat. No. 4,412,989), ribonuclease and superoxide dismutase (Veronese et al., *App. Biochem. Biotech.* 11: 141-52 (1985)). All references and patents cited are incorporated by reference herein.

PEGylation (i.e., addition of any water soluble polymer) of hPP or hA or hFc polypeptides containing a non-naturally encoded amino acid, such as p-azido-L-phenylalanine, is carried out by any convenient method. For example, hPP or hA or hFc polypeptide is PEGylated with an alkyne-terminated mPEG derivative. Briefly, an excess of solid mPEG(5000)-O-CH₂-C≡CH is added, with stirring, to an aqueous solution of p-azido-L-Phe-containing hPP or hA or hFc polypeptide at room temperature. Typically, the aqueous solution is buffered with a buffer having a pK_a near the pH at which the reaction is to be carried out (generally about pH 4-10). Examples of suitable buffers for PEGylation at pH 7.5, for instance, include, but are not limited to, HEPES, phosphate, borate, TRIS-HCl, EPPS, and TES. The pH is continuously monitored and adjusted if necessary. The reaction is typically allowed to continue for between about 1-48 hours.

The reaction products are subsequently subjected to hydrophobic interaction chromatography to separate the PEGylated hPP or hA or hFc polypeptide variants from free mPEG(5000)-O-CH₂-C≡CH and any high-molecular weight complexes of the pegylated hPP or hA or hFc polypeptide which may form when unblocked PEG is activated at both ends of the molecule, thereby crosslinking hPP or hA or hFc polypeptide variant molecules. The conditions during hydrophobic interaction chromatography are such that free mPEG(5000)-O-CH₂-C≡CH flows through the column, while any crosslinked PEGylated hPP or hA or hFc polypeptide variant complexes elute after the desired forms, which contain one hPP or hA or hFc polypeptide variant molecule conjugated to one or more PEG groups. Suitable conditions

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vary depending on the relative sizes of the cross-linked complexes versus the desired conjugates and are readily determined by those of ordinary skill in the art. The eluent containing the desired conjugates is concentrated by ultrafiltration and desalted by diafiltration.

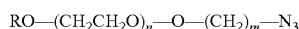
If necessary, the PEGylated hPP or hA or hFc polypeptide obtained from the hydrophobic chromatography can be purified further by one or more procedures known to those of ordinary skill in the art including, but are not limited to, affinity chromatography; anion- or cation-exchange chromatography (using, including but not limited to, DEAE SEPHAROSE); chromatography on silica; reverse phase HPLC; gel filtration (using, including but not limited to, SEPHADEX G-75); hydrophobic interaction chromatography; size-exclusion chromatography, metal-chelate chromatography; ultrafiltration/diafiltration; ethanol precipitation; ammonium sulfate precipitation; chromatofocusing; displacement chromatography; electrophoretic procedures (including but not limited to preparative iso electric focusing), differential solubility (including but not limited to ammonium sulfate precipitation), or extraction. Apparent molecular weight may be estimated by GPC by comparison to globular protein standards (Preneta, A Z in PROTEIN PURIFICATION METHODS, A PRACTICAL APPROACH (Harris & Angal, Eds.) IRL Press 1989, 293-306). The purity of the hPP or hA-PEG conjugate can be assessed by proteolytic degradation (including but not limited to, trypsin cleavage) followed by mass spectrometry analysis. Pepinsky R B., et al., J. Pharmacol. & Exp. Ther. 297(3):1059-66 (2001).

A water soluble polymer linked to an amino acid of an hPP or hA or hFc polypeptide of the invention can be further derivatized or substituted without limitation.

Azide-containing PEG Derivatives

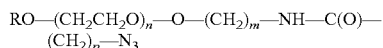
In another embodiment of the invention, an hPP or hA or hFc polypeptide is modified with a PEG derivative that contains an azide moiety that will react with an alkyne moiety present on the side chain of the non-naturally encoded amino acid. In general, the PEG derivatives will have an average molecular weight ranging from 1-100 kDa and, in some embodiments, from 10-40 kDa.

In some embodiments, the azide-terminal PEG derivative will have the structure:



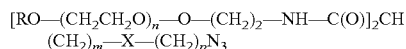
where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000 (i.e., average molecular weight is between 5-40 kDa).

In another embodiment, the azide-terminal PEG derivative will have the structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10, p is 2-10 and n is 100-1,000 (i.e., average molecular weight is between 5-40 kDa).

In another embodiment of the invention, an hPP or hA or hFc polypeptide comprising an alkyne-containing amino acid is modified with a branched PEG derivative that contains a terminal azide moiety, with each chain of the branched PEG having a MW ranging from 10-40 kDa and may be from 5-20 kDa. For instance, in some embodiments, the azide-terminal PEG derivative will have the following structure:



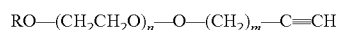
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where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10, p is 2-10, and n is 100-1,000, and X is optionally an O, N, S or carbonyl group (C=O), in each case that can be present or absent.

Alkyne-containing PEG Derivatives

In another embodiment of the invention, an hPP or hA or hFc polypeptide is modified with a PEG derivative that contains an alkyne moiety that will react with an azide moiety present on the side chain of the non-naturally encoded amino acid.

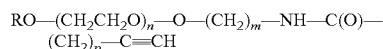
In some embodiments, the alkyne-terminal PEG derivative will have the following structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10 and n is 100-1,000 (i.e., average molecular weight is between 5-40 kDa).

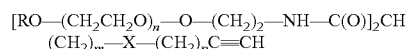
In another embodiment of the invention, an hPP or hA or hFc polypeptide comprising an alkyne-containing non-naturally encoded amino acid is modified with a PEG derivative that contains a terminal azide or terminal alkyne moiety that is linked to the PEG backbone by means of an amide linkage.

In some embodiments, the alkyne-terminal PEG derivative will have the following structure:



where R is a simple alkyl (methyl, ethyl, propyl, etc.), in is 2-10, p is 2-10 and n is 100-1,000.

In another embodiment of the invention, an hPP or hA or hFc polypeptide comprising an azide-containing amino acid is modified with a branched PEG derivative that contains a terminal alkyne moiety, with each chain of the branched PEG having a MW ranging from 10-40 kDa and may be from 5-20 kDa. For instance, in some embodiments, the alkyne-terminal PEG derivative will have the following structure:

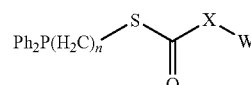


where R is a simple alkyl (methyl, ethyl, propyl, etc.), m is 2-10, p is 2-10, and n is 100-1,000, and X is optionally an O, N, S or carbonyl group (C=O), or not present.

Phosphine-containing PEG Derivatives

In another embodiment of the invention, an hPP or hA or hFc polypeptide is modified with a PEG derivative that contains an activated functional group (including but not limited to, ester, carbonate) further comprising an aryl phosphine group that will react with an azide moiety present on the side chain of the non-naturally encoded amino acid. In general, the PEG derivatives will have an average molecular weight ranging from 1-100 kDa and, in some embodiments, from 10-40 kDa.

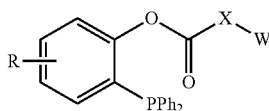
In some embodiments, the PEG derivative will have the structure:



wherein n is 1-10; X can be O, N, S or not present, Ph is phenyl, and W is a water soluble polymer.

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In some embodiments, the PEG derivative will have the structure:



wherein X can be O, N, S or not present, Ph is phenyl, W is a water soluble polymer and R can be H, alkyl, aryl, substituted alkyl and substituted aryl groups. Exemplary R groups include but are not limited to $-\text{CH}_2$, $-\text{C}(\text{CH}_3)_3$, $-\text{OR}'$, $-\text{NR}'\text{R}''$, $-\text{SR}'$, -halogen, $-\text{C}(\text{O})\text{R}'$, $-\text{CONR}'\text{R}''$, $-\text{S}(\text{O})_2\text{R}'$, $-\text{S}(\text{O})_2\text{NR}'\text{R}''$, $-\text{CN}$ and $-\text{NO}_2$. R' , R'' , R''' and R'''' each independently refer to hydrogen, substituted or unsubstituted heteroalkyl, substituted or unsubstituted aryl, including but not limited to, aryl substituted with 1-3 halogens, substituted or unsubstituted alkyl, alkoxy or thioalkoxy groups, or arylalkyl groups. When a compound of the invention includes more than one R group, for example, each of the R groups is independently selected as are each R' , R'' , R''' and R'''' groups when more than one of these groups is present. When R' and R'' are attached to the same nitrogen atom, they can be combined with the nitrogen atom to form a 5-, 6-, or 7-membered ring. For example, $-\text{NR}'\text{R}''$ is meant to include, but not be limited to, 1-pyrrolidinyl and 4-morpholinyl. From the above discussion of substituents, one of skill in the art will understand that the term "alkyl" is meant to include groups including carbon atoms bound to groups other than hydrogen groups, such as haloalkyl (including but not limited to, $-\text{CF}_3$ and $-\text{CH}_2\text{CF}_3$) and acyl (including but not limited to, $-\text{C}(\text{O})\text{CH}_3$, $-\text{C}(\text{O})\text{CF}_3$, $-\text{C}(\text{O})\text{CH}_2\text{OCH}_3$, and the like).

Other PEG Derivatives and General PEGylation Techniques

Other exemplary PEG molecules that may be linked to hPP or hA or hFc polypeptides, as well as PEGylation methods include those described in, e.g., U.S. Patent Publication No. 2004/0001838; 2002/0052009; 2003/0162949; 2004/0013637; 2003/0228274; 2003/0220447; 2003/0158333; 2003/0143596; 2003/0114647; 2003/0105275; 2003/0105224; 2003/0023023; 2002/0156047; 2002/0099133; 2002/0086939; 2002/0082345; 2002/0072573; 2002/0052430; 2002/0040076; 2002/0037949; 2002/0002250; 2001/0056171; 2001/0044526; 2001/0021763; U.S. Pat. Nos. 6,646,110; 5,824,778; 5,476,653; 5,219,564; 5,629,384; 5,736,625; 4,902,502; 5,281,698; 5,122,614; 5,473,034; 5,516,673; 5,382,657; 6,552,167; 6,610,281; 6,515,100; 6,461,603; 6,436,386; 6,214,966; 5,990,237; 5,900,461; 5,739,208; 5,672,662; 5,446,090; 5,808,096; 5,612,460; 5,324,844; 5,252,714; 6,420,339; 6,201,072; 6,451,346; 6,306,821; 5,559,213; 5,747,646; 5,834,594; 5,849,860; 5,980,948; 6,004,573; 6,129,912; WO 97/32607, EP 229, 108, EP 402,378, WO 92/16555, WO 94/04193, WO 94/14758, WO 94/17039, WO 94/18247, WO 94/28024, WO 95/00162, WO 95/11924, WO 95/13090, WO 95/33490, WO 96/00080, WO 97/18832, WO 98/41562, WO 98/48837, WO 99/32134, WO 99/32139, WO 99/32140, WO 96/40791, WO 98/32466, WO 95/06058, EP 439 508, WO 97/03106, WO 96/21469, WO 95/13312, EP 921 131, WO 98/05363, EP 809 996, WO 96/41813, WO 96/07670, EP 605 963, EP 510 356, EP 400 472, EP 183 503 and EP 154 316, which are incorporated by reference herein. Any of the PEG molecules described herein may be used in any form, including but not limited to, single chain, branched chain, multiarm chain, single functional, bi-functional, multi-functional, or any combination thereof.

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Enhancing Affinity of Biologically Active Molecules for hA

Various biologically active molecules can also be fused to the hA polypeptides of the invention to modulate the half-life of the biologically active molecule, or modulate another property of the biologically active molecule. In some embodiments, biologically active molecules are linked or fused to hA polypeptides of the invention to enhance affinity for endogenous binding partners.

For example, in some cases, a recombinant fusion of a biologically active molecule and hA is made. Exemplary albumin binding sequences include, but are not limited to, the albumin binding domain from streptococcal protein G (see, e.g., Makrides et al., *J. Pharmacol. Exp. Ther.* 277:534-542 (1996) and Sjolander et al., *J. Immunol. Methods* 201:115-123 (1997)), or albumin-binding peptides such as those described in, e.g., Dennis, et al., *J. Biol. Chem.* 277:35035-35043 (2002).

In other embodiments, the biologically active molecule of the present invention are acylated with fatty acids. In some cases, the fatty acids promote binding to hA. See, e.g., Kurtzhals, et al., *Biochem. J.* 312:725-731 (1995).

In other embodiments, the biologically active molecule polypeptides of the invention are fused directly with hA. Those of skill in the art will recognize that a wide variety of other biologically active molecules can also be linked to other hPP's in the present invention to modulate binding to binding partners.

X. Glycosylation of hPP or hA or hFc Polypeptides

The invention includes hPP or hA or hFc polypeptides incorporating one or more non-naturally encoded amino acids bearing saccharide residues. The saccharide residues may be either natural (including but not limited to, N-acetylglucosamine) or non-natural (including but not limited to, 3-fluorogalactose). The saccharides may be linked to the non-naturally encoded amino acids either by an N- or O-linked glycosidic linkage (including but not limited to, N-acetylglactose-L-serine) or a non-natural linkage (including but not limited to, an oxime or the corresponding C- or S-linked glycoside).

The saccharide (including but not limited to, glycosyl) moieties can be added to hPP or hA or hFc polypeptides either in vivo or in vitro. In some embodiments of the invention, an hPP or hA or hFc polypeptide comprising a carbonyl-containing non-naturally encoded amino acid is modified with a saccharide derivatized with an amino oxy group to generate the corresponding glycosylated polypeptide linked via an oxime linkage. Once attached to the non-naturally encoded amino acid, the saccharide may be further elaborated by treatment with glycosyltransferases and other enzymes to generate an oligosaccharide bound to the hPP or hA or hFc polypeptide. See, e.g., H. Liu, et al. *J. Am. Chem. Soc.* 125: 1702-1703 (2003).

In some embodiments of the invention, an hPP or hA or hFc polypeptide comprising a carbonyl-containing non-naturally encoded amino acid is modified directly with a glycan with defined structure prepared as an aminoxy derivative. One of ordinary skill in the art will recognize that other functionalities, including azide, alkyne, hydrazide, hydrazine, and semicarbazide, can be used to link the saccharide to the non-naturally encoded amino acid.

In some embodiments of the invention, an hPP or hA or hFc polypeptide comprising an azide or alkynyl-containing non-naturally encoded amino acid can then be modified by, including but not limited to, a Huisgen [3+2] cycloaddition reaction with, including but not limited to, alkynyl or azide derivatives, respectively. This method allows for proteins to be modified with extremely high selectivity.

XI. Measurement of Biologically Active Molecule Activity

Regardless of which methods are used to create the hPP or hA or hFc, they are subject to assays for biological activity. Tritiated thymidine assays may be conducted to ascertain the degree of cell division, if appropriate. Other biological assays, however, may be used to ascertain the desired activity. Biological assays such as measuring the ability to inhibit an antigen's biological activity, such as an enzymatic, proliferative, or metabolic activity also provides an indication of hPP or hFc activity. Other in vitro assays may be used to ascertain biological activity. In general, the test for biological activity should provide analysis for the desired result, such as increase or decrease in biological activity (as compared to non-altered hPP or hFc), different biological activity (as compared to non-altered hPP or hFc), receptor or binding partner affinity analysis, conformational or structural changes of the hPP or hFc itself or binding partner (as compared to the non-altered hPP or hFc), or serum half-life analysis, as appropriate for the antigen's biological activity.

The above compilation of references for assay methodologies is not exhaustive, and those of ordinary skill in the art will recognize other assays useful for testing for the desired end result.

XIII. Measurement of Potency, Functional In Vivo Half-life, and Pharmacokinetic Parameters

An important aspect of the invention is the prolonged biological half-life that is obtained by construction of the hPP or hA or hFc polypeptide with or without conjugation of the polypeptide to a water soluble polymer moiety. The rapid decrease of hPP or hA or hFc polypeptide serum concentrations has made it important to evaluate biological responses to treatment with conjugated and non-conjugated hPP or hA or hFc polypeptide and variants thereof. The conjugated and non-conjugated hPP or hA or hFc polypeptide and variants thereof of the present invention may have prolonged serum half-lives also after subcutaneous or i.v. administration, making it possible to measure by, e.g. ELISA method or by a primary screening assay. ELISA or RIA kits from either BioSource International (Camarillo, Calif.) or Diagnostic Systems Laboratories (Webster, Tex.) may be used. Measurement of in vivo biological half-life is carried out as described herein.

The potency and functional in vivo half-life of an hPP or hA or hFc polypeptide comprising a non-naturally encoded amino acid can be determined according to the protocol described in Clark, R., et al., *J. Biol. Chem.* 271(36): 21969-21977 (1996).

Pharmacokinetic parameters for an hPP or hA or hFc polypeptide comprising a non-naturally encoded amino acid can be evaluated in normal Sprague-Dawley male rats (N=5 animals per treatment group). Animals will receive either a single dose of 25 ug/rat iv or 50 ug/rat sc, and approximately 5-7 blood samples will be taken according to a pre-defined time course, generally covering about 6 hours for an hPP or hA or hFc polypeptide comprising a non-naturally encoded amino acid not conjugated to a water soluble polymer and about 4 days for an hPP or hA polypeptide comprising a non-naturally encoded amino acid and conjugated to a water soluble polymer. Pharmacokinetic data for hPP or hA or hFc polypeptides is well-studied in several species and can be compared directly to the data obtained for hPP or hA or hFc polypeptides comprising a non-naturally encoded amino acid. See Mordenti J., et al., *Pharm. Res.* 8(11):1351-59 (1991) for studies related to hPP or hA or hFc.

Pharmacokinetic parameters can also be evaluated in a primate, e.g., cynomolgus monkeys. Typically, a single injection

is administered either subcutaneously or intravenously, and serum hPP or hA or hFc levels are monitored over time.

The specific activity of hPP or hA or hFc polypeptides in accordance with this invention can be determined by various assays known in the art. The biological activity of the hPP or hA or hFc polypeptide muteins, or fragments thereof, obtained and purified in accordance with this invention can be tested by methods described or referenced herein or known to those of ordinary skill in the art.

XIV. Administration and Pharmaceutical Compositions

The polypeptides or proteins of the invention (including but not limited to, hPP or hA or hFc, synthetases, proteins comprising one or more unnatural amino acid, etc.) are optionally employed for therapeutic uses, including but not limited to, in combination with a suitable pharmaceutical carrier. Such compositions, for example, comprise a therapeutically effective amount of the compound, and a pharmaceutically acceptable carrier or excipient. Such a carrier or excipient includes, but is not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and/or combinations thereof. The formulation is made to suit the mode of administration. In general, methods of administering proteins are known to those of ordinary skill in the art and can be applied to administration of the polypeptides of the invention.

Therapeutic compositions comprising one or more polypeptide of the invention are optionally tested in one or more appropriate in vitro and/or in vivo animal models of disease, to confirm efficacy, tissue metabolism, and to estimate dosages, according to methods known to those of ordinary skill in the art. In particular, dosages can be initially determined by activity, stability or other suitable measures of unnatural herein to natural amino acid homologues (including but not limited to, comparison of an hPP or hA or hFc polypeptide modified to include one or more unnatural amino acids to a natural amino acid hPP or hA or hFc polypeptide), i.e., in a relevant assay.

Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells. The unnatural amino acid polypeptides of the invention are administered in any suitable manner, optionally with one or more pharmaceutically acceptable carriers. Suitable methods of administering such polypeptides in the context of the present invention to a patient are available, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective action or reaction than another route.

Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention.

hPP or hA or hFc polypeptides of the invention may be administered by any conventional route suitable for proteins or peptides, including, but not limited to parenterally, e.g. injections including, but not limited to, subcutaneously or intravenously or any other form of injections or infusions. Polypeptide compositions can be administered by a number of routes including, but not limited to oral, intravenous, intraperitoneal, intramuscular, ophthalmic, intraocular, intracranial, subdural, into the CSF, transdermal, subcutaneous, topical, sublingual, or rectal means. Compositions comprising non-natural amino acid polypeptides, modified or unmodified, can also be administered via liposomes. Such administration routes and appropriate formulations are generally known to those of skill in the art. The hPP or hA or hFc

polypeptide comprising a non-naturally encoded amino acid, may be used alone or in combination with other suitable components such as a pharmaceutical carrier. The hPP or hA or hFc polypeptide comprising a non-naturally encoded amino acid, may also be used in combination with a pharmaceutical carrier that is biodegradable or biosoluble for modulated release or availability of the active agent.

The hPP or hA or hFc polypeptide comprising a non-natural amino acid, alone or in combination with other suitable components, can also be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

Formulations suitable for parenteral administration, such as, for example, by intraarticular (in the joints), intravenous, intramuscular, intradermal, intraperitoneal, intraocular, intracranial, and subcutaneous routes, include aqueous and non-aqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. The formulations of hPP or hA or hFc can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials.

Parenteral administration and intravenous administration are preferred methods of administration. In particular, the routes of administration already in use for natural amino acid homologue therapeutics (including but not limited to, those typically used for albumin, albumin fusions with other polypeptides, EPO, GH, G-CSF, GM-CSF, IFNs, interleukins, antibodies, antibody fragments, and/or any other pharmaceutically delivered protein), along with formulations in current use, provide preferred routes of administration and formulation for the polypeptides of the invention.

The dose administered to a patient, in the context of the present invention, is sufficient to have a beneficial therapeutic response in the patient over time, depending on the application. The dose is determined by the efficacy of the particular vector, or formulation, and the activity, stability or serum half-life of the unnatural amino acid polypeptide employed and the condition of the patient, as well as the body weight or surface area of the patient to be treated. The size of the dose is also determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular vector, formulation, or the like in a particular patient.

In determining the effective amount of the vector or formulation to be administered in the treatment or prophylaxis of disease (including but not limited to, cancers, inherited diseases, diabetes, AIDS, or the like), the physician evaluates circulating plasma levels, formulation toxicities, progression of the disease, and/or where relevant, the production of anti-unnatural amino acid polypeptide antibodies.

The dose administered, for example, to a 70 kilogram patient, is typically in the range equivalent to dosages of currently-used therapeutic proteins, adjusted for the altered activity or serum half-life of the relevant composition. The vectors or pharmaceutical formulations of this invention can supplement treatment conditions by any known conventional therapy, including antibody administration, vaccine administration, administration of cytotoxic agents, natural amino acid polypeptides, nucleic acids, nucleotide analogues, biologic response modifiers, and the like.

For administration, formulations of the present invention are administered at a rate determined by the LD-50 or ED-50

of the relevant formulation, and/or observation of any side-effects of the unnatural amino acid polypeptides at various concentrations, including but not limited to, as applied to the mass and overall health of the patient. Administration can be accomplished via single or divided doses.

If a patient undergoing infusion of a formulation develops fevers, chills, or muscle aches, he/she receives the appropriate dose of aspirin, ibuprofen, acetaminophen or other pain/fever controlling drug. Patients who experience reactions to the infusion such as fever, muscle aches, and chills are premedicated 30 minutes prior to the future infusions with either aspirin, acetaminophen, or, including but not limited to, diphenhydramine. Meperidine is used for more severe chills and muscle aches that do not quickly respond to antipyretics and antihistamines. Cell infusion is slowed or discontinued depending upon the severity of the reaction.

The hPP or hA or hFc polypeptides of the invention can be administered directly to a mammalian subject. Administration is by any of the routes normally used for introducing hPP or hA or hFc polypeptide to a subject. The hPP or hA or hFc polypeptide compositions according to embodiments of the present invention include those suitable for oral, rectal, topical, inhalation (including but not limited to, via an aerosol), buccal (including but not limited to, sub-lingual), vaginal, parenteral (including but not limited to, subcutaneous, intramuscular, intradermal, intraarticular, intrapleural, intraperitoneal, intracerebral, intraarterial, or intravenous), topical (i.e., both skin and mucosal surfaces, including airway surfaces) and transdermal administration, although the most suitable route in any given case will depend on the nature and severity of the condition being treated. Administration can be either local or systemic. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampoules and vials. The hPP or hA or hFc polypeptides of the invention can be prepared in a mixture in a unit dosage injectable form (including but not limited to, solution, suspension, or emulsion) with a pharmaceutically acceptable carrier. The hPP or hA or hFc polypeptides of the invention can also be administered by continuous infusion (using, including but not limited to, minipumps such as osmotic pumps), single bolus or slow-release depot formulations.

Formulations suitable for administration include aqueous and non-aqueous solutions, isotonic sterile solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. Solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described.

Freeze-drying is a commonly employed technique for presenting proteins which serves to remove water from the protein preparation of interest. Freeze-drying, or lyophilization, is a process by which the material to be dried is first frozen and then the ice or frozen solvent is removed by sublimation in a vacuum environment. An excipient may be included in pre-lyophilized formulations to enhance stability during the freeze-drying process and/or to improve stability of the lyophilized product upon storage. Pikal, M. *Biopharm.* 3(9):26-30 (1990) and Arakawa et al. *Pharm. Res.* 8(3):285-291 (1991).

The spray drying of pharmaceuticals is also known to those of ordinary skill in the art. For example, see Broadhead, J. et al., "The Spray Drying of Pharmaceuticals," in *Drug Dev. Ind. Pharm.* 18 (11 & 12), 1169-1206 (1992). In addition to small molecule pharmaceuticals, a variety of biological materials have been spray dried and these include: enzymes, sera,

plasma, micro-organisms and yeasts. Spray drying is a useful technique because it can convert a liquid pharmaceutical preparation into a fine, dustless or agglomerated powder in a one-step process. The basic technique comprises the following four steps: a) atomization of the feed solution into a spray; b) spray-air contact; c) drying of the spray; and d) separation of the dried product from the drying air. U.S. Pat. Nos. 6,235,710 and 6,001,800, which are incorporated by reference herein, describe the preparation of recombinant erythropoietin by spray drying.

The pharmaceutical compositions and formulations of the invention may comprise a pharmaceutically acceptable carrier, excipient, or stabilizer. Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions (including optional pharmaceutically acceptable carriers, excipients, or stabilizers) of the present invention (see, e.g., *Remington's Pharmaceutical Sciences*, 17th ed. 1985).

Suitable carriers include but are not limited to, buffers containing succinate, phosphate, borate, HEPES, citrate, histidine, imidazole, acetate, bicarbonate, and other organic acids; antioxidants including but not limited to, ascorbic acid; low molecular weight polypeptides including but not limited to those less than about 10 residues; proteins, including but not limited to, serum albumin, gelatin, or immunoglobulins; hydrophilic polymers including but not limited to, polyvinylpyrrolidone; amino acids including but not limited to, glycine, glutamine, asparagine, arginine, histidine or histidine derivatives, methionine, glutamate, or lysine; monosaccharides, disaccharides, and other carbohydrates, including but not limited to, trehalose, sucrose, glucose, mannose, or dextrans; chelating agents including but not limited to, EDTA and edentate disodium; divalent metal ions including but not limited to, zinc, cobalt, or copper; sugar alcohols including but not limited to, mannitol or sorbitol; salt-forming counter ions including but not limited to, sodium and sodium chloride; and/or nonionic surfactants including but not limited to TweenTM (including but not limited to, Tween 80 (polysorbate 80) and Tween 20 (polysorbate 20), PluronicTM and other pluronic acids, including but not limited to, pluronic acid F68 (poloxamer 188), or PEG. Suitable surfactants include for example but are not limited to polyethers based upon polyethylene oxide)-poly(propylene oxide)-poly(ethylene oxide), i.e., (PEO-PPO-PEO), or poly(propylene oxide)-poly(ethylene oxide)-poly(propylene oxide), i.e., (PPO-PEO-PPO), or a combination thereof. PEO-PPO-PEO and PPO-PEO-PPO are commercially available under the trade names PluronicTM, R-PluronicTM, TetronicsTM and R-TetronicsTM (BASF Wyandotte Corp., Wyandotte, Mich.) and are further described in U.S. Pat. No. 4,820,352 incorporated herein in its entirety by reference. Other ethylene/polypropylene block polymers may be suitable surfactants. A surfactant or a combination of surfactants may be used to stabilize PEGylated hPP or hA or hFc against one or more stresses including but not limited to stress that results from agitation. Some of the above may be referred to as "bulking agents." Some may also be referred to as "tonicity modifiers." Antimicrobial preservatives may also be applied for product stability and antimicrobial effectiveness; suitable preservatives include but are not limited to, benzyl alcohol, benzalkonium chloride, metacresol, methyl/propyl paraben, cresol, and phenol, or a combination thereof.

hPP or hA or hFc polypeptides of the invention, including those linked to water soluble polymers such as PEG can also be administered by or as part of sustained-release systems.

Sustained-release compositions include, including but not limited to, semi-permeable polymer matrices in the form of shaped articles, including but not limited to, films, or microcapsules. Sustained-release matrices include from biocompatible materials such as poly(2-hydroxyethyl methacrylate) (Langer et al., *J. Biomed. Mater. Res.*, 15: 267-277 (1981); Langer, *Chem. Tech.*, 12: 98-105 (1982), ethylene vinyl acetate (Langer et al., *supra*) or poly-D(-)-3-hydroxybutyric acid (EP 133,988), polylactides (polylactic acid) (U.S. Pat. No. 3,773,919; EP 58,481), polyglycolide (polymer of glycolic acid), polylactide co-glycolide (copolymers of lactic acid and glycolic acid) polyanhydrides, copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., *Biopolymers*, 22, 547-556 (1983), poly(ortho)esters, polypeptides, hyaluronic acid, collagen, chondroitin sulfate, carboxylic acids, fatty acids, phospholipids, polysaccharides, nucleic acids, polyamino acids, amino acids such as phenylalanine, tyrosine, isoleucine, polynucleotides, polyvinyl propylene, polyvinylpyrrolidone and silicone. Sustained-release compositions also include a liposomally entrapped compound. Liposomes containing the compound are prepared by methods known per se: DE 3,218,121; Eppstein et al., *Proc. Natl. Acad. Sci. U.S.A.*, 82: 3688-3692 (1985); Hwang et al., *Proc. Natl. Acad. Sci. U.S.A.*, 77: 4030-4034 (1980); EP 52,322; EP 36,676; U.S. Pat. No. 4,619,794; EP 143,949; U.S. Pat. No. 5,021,234; Japanese Pat. Appln. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. All references and patents cited are incorporated by reference herein.

Liposomally entrapped hPP or hA or hFc polypeptides can be prepared by methods described in, e.g., DE 3,218,121; Eppstein et al., *Proc. Natl. Acad. Sci. U.S.A.*, 82: 3688-3692 (1985); Hwang et al., *Proc. Natl. Acad. Sci. U.S.A.*, 77: 4030-4034 (1980); EP 52,322; EP 36,676; U.S. Pat. No. 4,619,794; EP 143,949; U.S. Pat. No. 5,021,234; Japanese Pat. Appln. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Composition and size of liposomes are well known or able to be readily determined empirically by one of ordinary skill in the art. Some examples of liposomes as described in, e.g., Park J W, et al., *Proc. Natl. Acad. Sci. USA* 92:1327-1331 (1995); Lasic D and Papahadjopoulos D (eds): *MEDICAL APPLICATIONS OF LIPOSOMES* (1998); Drummond D C, et al., *Liposomal drug delivery systems for cancer therapy*, in Teicher B (ed): *CANCER DRUG DISCOVERY AND DEVELOPMENT* (2002); Park J W, et al., *Clin. Cancer Res.* 8:1172-1181 (2002); Nielsen U B, et al., *Biochim. Biophys. Acta* 1591(1-3):109-118 (2002); Mamot C, et al., *Cancer Res.* 63: 3154-3161 (2003). All references and patents cited are incorporated by reference herein.

The dose administered to a patient in the context of the present invention should be sufficient to cause a beneficial response in the subject over time. Generally, the total pharmaceutically effective amount of the hPP or hA or hFc polypeptide of the present invention administered parenterally per dose is in the range of about 0.01 µg/kg/day to about 100 µg/kg, or about 0.05 mg/kg to about 1 mg/kg, of patient body weight, although this is subject to therapeutic discretion. The frequency of dosing is also subject to therapeutic discretion, and may be more frequent or less frequent than the commercially available hPP or hA or hFc polypeptide products approved for use in humans. Generally, a PEGylated hPP or hA or hFc polypeptide of the invention can be administered by any of the routes of administration described above.

The following examples are offered to illustrate, but do not to limit the claimed invention.

Example 1

This example describes one of the many potential sets of criteria for the selection of preferred sites of incorporation of non-naturally encoded amino acids into hA. Using the criteria described below, the amino acid positions utilized for site-specific incorporation of p-acetyl-phenylalanine (pAF) into HSA are NO: 34, 82, 172, 301, 364, 505. Several HSA crystal structures were used to determine preferred positions into which one or more non-naturally encoded amino acids could be introduced: the coordinates for these structures are available from the Protein Data Bank (PDB) via The Research Collaboratory for Structural Bioinformatics at www.rcsb.org

(PDB IDs 1A06, 1E78 and 1BMO). X-ray crystal structure information was used to perform solvent accessibility calculations on the HSA molecule, utilizing the Cx program (Pintar et al. *Bioinformatics*, 2002, Vol. 18, p 980). The solvent accessibility of all atoms was calculated and a composite Cx value for each amino acid residue was determined, and is shown in FIG. 1. Amino acids were rank-ordered by Cx value and correlated with their 3-dimensional position in the HSA structure, and certain of these sites are shown on FIG. 2. HSA contains a total of 582 amino acids: the top 51 Cx values were examined for pAF substitution. Sites were chosen in order to place pAF into solvent-exposed regions of the HSA structure where covalent conjugation would be most feasible. The following criteria were used to evaluate the top 51 Cx positions of HSA for the introduction of a non-naturally encoded amino acid: the selected residues (a) should have a maximal Cx value, demonstrating solvent-accessibility and minimal van der Waals or hydrogen bonding interactions with surrounding residues, b) should be from different surface-exposed regions

of the protein and c) should be in areas of both rigid and flexible protein structure. A partial listing of amino acid positions suitable for incorporation of non-naturally encoded amino acids into hA are shown in FIG. 3.

Example 2

This example details cloning and expression of a hA polypeptide with and without a non-naturally encoded amino acid in yeast. [Cloning of the albumin DNA into expression vector, transformation of yeast]

An introduced translation system that comprises an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS) is used to express hA containing a non-naturally encoded amino acid. The O-RS preferentially aminoacylates the O-tRNA with a non-naturally encoded amino acid. In turn the translation system inserts the non-naturally encoded amino acid into hA, in response to an encoded selector codon.

TABLE 2

hA, O-RS and O-tRNA sequences.		
SEQ ID NO: 1	Human albumin amino acid sequence	hA
SEQ ID NO: 2	Nucleotide sequence encoding human albumin	hA
SEQ ID NO: 3	<i>M. jannaschii</i> mtRNA _{CUA} ^{Tyr}	tRNA
SEQ ID NO: 4	HLAD03; an optimized amber suppressor tRNA	tRNA
SEQ ID NO: 5	HL325A; an optimized AGGA frameshift suppressor tRNA	tRNA
SEQ ID NO: 6	Aminoacyl tRNA synthetase for the incorporation of p-azido-L-phenylalanine p-Az-PheRS(6)	RS
SEQ ID NO: 7	Aminoacyl tRNA synthetase for the incorporation of p-benzoyl-L-phenylalanine p-BpaRS(1)	RS
SEQ ID NO: 8	Aminoacyl tRNA synthetase for the incorporation of propargyl-phenylalanine Propargyl-PheRS	RS
SEQ ID NO: 9	Aminoacyl tRNA synthetase for the incorporation of propargyl-phenylalanine Propargyl-PheRS	RS
SEQ ID NO: 10	Aminoacyl tRNA synthetase for the incorporation of propargyl-phenylalanine Propargyl-PheRS	RS
SEQ ID NO: 11	Aminoacyl tRNA synthetase for the incorporation of p-azido-phenylalanine p-Az-PheRS(1)	RS
SEQ ID NO: 12	Aminoacyl tRNA synthetase for the incorporation of p-azido-phenylalanine p-Az-PheRS(3)	RS
SEQ ID NO: 13	Aminoacyl tRNA synthetase for the incorporation of p-azido-phenylalanine p-Az-PheRS(4)	RS
SEQ ID NO: 14	Aminoacyl tRNA synthetase for the incorporation of p-azido-phenylalanine p-Az-PheRS(2)	RS
SEQ ID NO: 15	Aminoacyl tRNA synthetase for the incorporation of p-acetyl-phenylalanine (LW1)	RS
SEQ ID NO: 16	Aminoacyl tRNA synthetase for the incorporation of p-acetyl-phenylalanine (LW5)	RS
SEQ ID NO: 17	Aminoacyl tRNA synthetase for the incorporation of p-acetyl-phenylalanine (LW6)	RS
SEQ ID NO: 18	Aminoacyl tRNA synthetase for the incorporation of p-azido-phenylalanine (AzPheRS-5)	RS
SEQ ID NO: 19	Aminoacyl tRNA synthetase for the incorporation of p-azido-phenylalanine (AzPheRS-6)	RS

The transformation of yeast with plasmids containing the modified hA gene and the orthogonal aminoacyl tRNA synthetase/tRNA pair (specific for the desired non-naturally encoded amino acid) allows the site-specific incorporation of non-naturally encoded amino acid into the hA polypeptide. The transformed yeast, grown at 37° C. in media containing between 0.01-100 mM of the particular non-naturally encoded amino acid, expresses modified hA with high fidelity and efficiency.

Saccharomyces cerevisiae strain MaV203 carrying either pGADHSA or pGADGAL4(control) were cultured 23 hours in YPD. Cells and supernatants were harvested by centrifugation at 4000 g for 5 minutes at 4° C. Cell extracts were generated by lysis of about 10 mg wet cell pellet. Supernatants were concentrated approximately 30x by 10 kDa MWCO spin columns 16 µl of reduced sample loaded into each well of a 4-12% Bis-Tris PAGE gel, run 50 minutes at 200V and either stained with Coomassie blue or transferred to nitrocellulose membrane (25V, 70 minutes). Blot was probed

with anti-HSA IgY pAb (200 ng/ml) primary and HRP-conjugated goat anti-IgY IgG (10 ng/ml), then detected using Supersignal ECL substrate (Sigma) and Biorad Fluor-S imaging system. The results are shown in FIG. 4.

Methods for purification of hA are known to those of ordinary skill in the art and are confirmed by SDS-PAGE, Western Blot analyses, or electrospray-ionization ion trap mass spectrometry and the like.

Cloning of the Albumin DNA into Expression Vector, Transformation of Yeast

The wildtype hA coding sequence (CDS) was cloned into yeast shuttle/expression vector pGADGAL4 as follows. Commercially available hA cDNA was obtained and amplified by PCR using primers specific for the 5' and 3' end of the hA CDS; HindIII restriction sites were integrated into the primer ends. Following PCR, the correct fragment was digested with HindIII (37° C., 60 minutes), purified, and ligated to HindIII-cut pGADGAL4. Ligation products were transformed into TOP10 chemically competent *E. coli*; plasmid DNA was isolated from selected transformants using a miniprep kit. Screening for the desired plasmid product was carried out by independent EcoRV and PstI restriction digests of each selected plasmid clone; those clones exhibiting the expected banding pattern following agarose gel electrophoresis (130V, 30 minutes) and EtBr staining were verified by sequencing. Clones were considered 'positive' if they had a copy of the hA CDS replacing the GAL4 region of pGADGAL4; the specific plasmid to be used in further experiments was named 'pGADHSA'.

Amber mutations were made to the specified codons within the hA CDS by the Quickchange method of site-directed mutagenesis (Stratagene, La Jolla, Calif.). Briefly, overlapping primers specific for the region to be mutated and containing the nucleotide-base changes necessary to generate it, were used in a PCR reaction to generate semi-mutated hybrid plasmid DNA molecules. Following DpnI restriction digestion to cleave and destroy the parental, methylated DNA strands, the products were transformed into TOP10 chemically competent *E. coli*. Transformants were selected; plasmid DNA was isolated and plasmid DNA containing the desired mutations were confirmed by nucleotide sequencing.

Saccharomyces cerevisiae transformations were carried out according to protocols detailed by R. D. Geitz (<http://www.umanitoba.ca/faculties/medicine/biochem/geitz/Trafo.html>). Briefly, freshly grown *S. cerevisiae* were scraped from YPD-agar plates in approximately 50 microliter aliquots, washed with sterile water, and resuspended in a transformation mix containing 33% poly(ethylene glycol)-3350, 100 mM LiOAc, 300 microgram/ml single stranded salmon sperm DNA, and 5-10 micrograms transforming plasmid DNA). Cells were heat-shocked for 40-60 minutes at 42° C., washed and resuspended in 1.0 ml sterile water, and plated in dilutions onto selective agar plates. Transformants were then used in subsequent expression and suppression experiments.

Expression and characterization of the HSA protein with non-natural amino acid.

Saccharomyces cerevisiae strain InvScl was transformed with either:

- 1.) pGADHSA(amber) alone,
- 2.) pGADHSA(amber) plus plasmid containing the *E. coli* tyrosine tRNA synthetase gene and the tRNA_{CUA} gene,
- 3.) pGADHSA(amber) plus plasmid containing the *E. coli* para-acetylphenylalanine tRNA synthetase gene and the tRNA_{CUA} gene.

Transformants were cultured in 50 ml SD media (lacking leucine, lacking tryptophan), and in the case of (3) above, in the presence of 1 mM para-acetylphenylalanine, at 30° C.

with shaking, to an OD₆₀₀ of 1.0. At this point, 30 OD₆₀₀ equivalents from each culture were pelleted by centrifugation at 3000×g for 5 minutes and resuspended in 30 ml YPD (again, in the case of (3) above, also in the presence of 1 mM para-acetylphenylalanine). Cultures were again allowed to grow at 30 degrees C. at 250 rpm shaking for a further 24 hours. 50 OD₆₀₀ equivalents from each culture were then pelleted as above; the culture supernatant was isolated, and a fraction of it was concentrated roughly 30-fold using a 10-kDa MWCO spin column.

The presence of hA protein was assayed by immunoblot, and is described as follows. 16 µl of each reduced sample was loaded into each well of a 4-12% Bis-Tris PAGE gel, run 50 minutes at 200V and either stained with Coomassie blue or transferred to nitrocellulose membrane (25V, 70 minutes). Blot was probed with anti-HSA IgY pAb (200 ng/ml) primary and HRP-conjugated goat anti-IgY IgG (10 ng/ml), then detected using Supersignal ECL substrate (Sigma) and Biorad Fluor-S imaging system. The results are shown in FIG. 5, and demonstrate incorporation of a non-naturally encoded amino acid into the hA polypeptide.

Non-naturally Encoded Amino Acid Suppression of HSA-C34

The *S. cerevisiae* Y187 strains transformed with plasmids encoding WT HSA, HSA-C34 or HSA-C34 plus a plasmid encoding a tRNA synthetase (RS)/tRNA pair [tyrosine (Y)RS, pAFRS, pAZRS, pBzRS, OMeRS] were grown in HC-Leu media or HC-Leu-Trp media overnight (30° C., 200 rpm). Cells were pelleted at 5000×g for 5 min at 4° C. and resuspended in YPAD to an OD₆₀₀ of 0.5. Strains containing an exogenous tRNA/RS pair were incubated in the presence (+) or absence (-) of the appropriate novel amino acid (pAF, pAZ-Phe, pBz-Phe, OMe-Tyr, 1 mM). pAF=para-acetylphenylalanine; pAZ-Phe=para-azidophenylalanine; pBz-Phe=para-benzoyl-L-phenylalanine; OMe-Tyr=O-methyltyrosine. Following a 24 hour incubation (30° C., 200 rpm), all cultures were harvested by centrifugation; 15 mL of reduced supernatant was resolved by SDS-PAGE with a 4-12% Bis-Tris gel and visualized by (FIG. 8A) Coomassie and (FIGS. 8B and C) anti-HSA Western blot. HSA Std is 200 ng HSA purified from human serum.

Conjugation of HSA-C34-pAF to 5K Amino-oxyPEG

Purified wt HSA or HSA-C34-pAF was buffer-exchanged into reaction buffer (20 mM sodium acetate, 20 g/L glycine, 5 g/L mannitol, 1 mM EDTA, pH 4.0), at a final concentration of ~2 mg/ml. Reactions on HSA-C34-pAF were initiated either with the addition of 20 molar equivalents of 5K amino-oxy derivatized PEG (+) or with the addition of reaction buffer (-); acetic hydrazide (catalyst: 50 mM final concentration) was added to all reactions. Reactions were allowed to proceed undisturbed at 28° C. for 48 hours. 1 µl of reaction mix per lane was then separated on a 4-12% bis-tris polyacrylamide gel and analyzed by α-HSA western blot. See FIG. 9. HSA Analytical Methods

Trypsinization of Samples

WT HSA (Sigma-Aldrich, 2 mg/ml) or purified, pAF-suppressed HSA (~2 mg/ml) was diluted into 6M guanidine-HCl and 50 mM Tris pH 7.5 (final concentration). Samples were reduced with 20 mM DTT at 37° C. for 1 hour followed by alkylation with 40 mM iodoacetic acid (IAA) for 40 minutes at room temperature in the dark. The reaction was quenched with 40 mM DTT, and samples were dialyzed into 50 mM Tris, 1 mM CaCl₂ pH 7.5 and treated with trypsin 1:20 (enzyme:protein) for 4 hours at 37° C. The reaction was quenched with addition of TFA to 0.1%.

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LC-MS/MS:

100 μ L of trypsinized sample was loaded onto a Zorbax SB-C18 column (2.1 \times 150 mm 3.5 μ m, 40° C.), at 0.2 mL/min. Peptides were eluted in 0.05% TFA with a 1.38%/min gradient of 0 to 100% acetonitrile over 60 minutes. Eluted peptides were electrosprayed directly onto a Thermo-Electron LCQ Deca with the application of 15V capillary voltage and 4.5 kV spray voltage. A cycle of one full-scan mass spectrum (300-2000 m/z) followed by data-dependent tandem MS spectra acquisition was performed at a 35% normalized collision energy throughout peptide elution. Peptide Mass Map of HSA-C34pAF

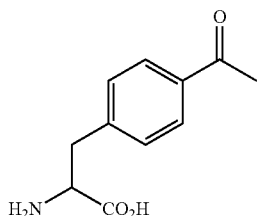
Purified wt HSA and HSA-C34pAF (approx. 60 μ g) were subjected to proteolytic digestion with trypsin, and LC-MS/MS was performed on samples with an LCQ Deca (Thermo-electron) to obtain a peptide mass map. Based on sequence analysis, the fifth tryptic peptide from the N-terminus (T5) in WT HSA contains Cys34; T5 in pAF-suppressed HSA should exhibit a mass difference corresponding to the Cys34pAF amino acid substitution. The WT T5 peptide (calculated M2H+ m/z=1246.95) eluted from the reverse phase column at 37.3 minutes with an observed m/z of 1246.4; the tryptic mass map of HSA-C34pAF at 37.3 minutes did not yield a peptide of m/z of 1246 \pm 2. Conversely, pAF-substituted T5 (calculated M2H+ m/z=1260.63) eluted at 39.1 minutes with an observed m/z of 1260.4 (FIG. 10, Panel A). No peptide with m/z=1246 \pm 2 was observed in the tryptic mass map of wt HSA at 39.1 minutes (FIG. 10, Panel B). The 39.1 min peak in (A) (m/z=1260.4) has an MS/MS spectrum consistent with the expected pAF-substituted T5 peptide (see FIG. 11). MS/MS of pAF-containing HSA Polypeptide

MS/MS spectrum of pAF-T5 parent ion (m/z=1260.4). Singly-charged ion fragments were produced by collision-induced dissociation of the doubly-charged parent ion. Peaks corresponding to predicted ink intervals (y" series) are indicated in the spectrum. The peak intervals are consistent with the HSA T5 peptide containing a Cys34-pAF substitution. See FIG. 11.

Example 3

This example details introduction of a carbonyl-containing amino acid and subsequent reaction with an aminooxy-containing PEG.

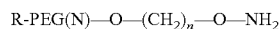
This Example demonstrates a method for the generation of a hA polypeptide that incorporates a ketone-containing non-naturally encoded amino acid that is subsequently reacted with an aminooxy-containing PEG of approximately 5,000 MW. Each of the residues 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581, identified according to the criteria of Example 1 (hA) is separately substituted with a non-naturally encoded amino acid having the following structure:



The sequences utilized for site-specific incorporation of p-acetyl-phenylalanine into hA are SEQ ID NO: 1.

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The hA polypeptide variant comprising the carbonyl-containing amino acid is reacted with an aminooxy-containing PEG derivative of the form:

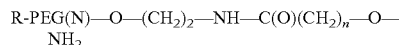


where R is methyl, n is 3 and N is approximately 5,000 MW. Another PEG derivative that is conjugated to hA has a molecular weight of 30,000. The purified hA containing p-acetylphenylalanine dissolved at 10 mg/mL in 25 mM MES (Sigma Chemical, St. Louis, Mo.) pH 6.0, 25 mM Hepes (Sigma Chemical, St. Louis, Mo.) pH 7.0, or in 10 mM Sodium Acetate (Sigma Chemical, St. Louis, Mo.) pH 4.5, is reacted with a 10 to 100-fold excess of aminooxy-containing PEG, and then stirred for 10-16 hours at room temperature (Jencks, W. J. *Am. Chem. Soc.* 1959, 81, pp 475). The PEG-hA is then diluted into appropriate buffer for immediate purification and analysis.

Example 4

Conjugation with a PEG consisting of a hydroxylamine group linked to the PEG via an amide linkage.

A PEG reagent having the following structure is coupled to a ketone-containing non-naturally encoded amino acid using the procedure described in Example 3:



where R=methyl, n=4 and N is approximately 20,000 MW. The reaction, purification, and analysis conditions are as described in Example 3.

Example 5

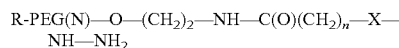
This example details the introduction of two distinct non-naturally encoded amino acids into hA polypeptides.

This example demonstrates a method for the generation of a hA polypeptide that incorporates non-naturally encoded amino acid comprising a ketone functionality at two positions among the following residues: E30, E74, Y103, K38, K41, K140, and K145. The hA polypeptide is prepared as described in Examples 1 and 2, except that the selector codon is introduced at two distinct sites within the nucleic acid.

Example 6

This example details conjugation of hA polypeptide to a hydrazide-containing PEG and subsequent in situ reduction.

A hA polypeptide incorporating a carbonyl-containing amino acid is prepared according to the procedure described in Examples 2 and 3. Once modified, a hydrazide-containing PEG having the following structure is conjugated to the hA polypeptide:



where R=methyl, n=2 and N=10,000 MW and X is a carbonyl (C=O) group. The purified hA containing p-acetylphenylalanine is dissolved at between 0.1-10 mg/mL in 25 mM MES (Sigma Chemical, St. Louis, Mo.) pH 6.0, 25 mM Hepes (Sigma Chemical, St. Louis, Mo.) pH 7.0, or in 10 mM Sodium Acetate (Sigma Chemical, St. Louis, Mo.) pH 4.5, is reacted with a 1 to 100-fold excess of hydrazide-containing PEG, and the corresponding hydrazone is reduced in situ by addition of stock 1M NaCNBH₃ (Sigma Chemical, St. Louis, Mo.), dissolved in H₂O, to a final concentration of 10-50 mM. Reactions are carried out in the dark at 4° C. to RT for 18-24 hours. Reactions are stopped by addition of 1 M Tris (Sigma

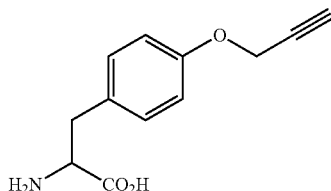
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Chemical, St. Louis, Mo.) at about pH 7.6 to a final Tris concentration of 50 mM or diluted into appropriate buffer for immediate purification.

Example 7

This example details introduction of an alkyne-containing amino acid into a hA polypeptide and derivatization with mPEG-azide.

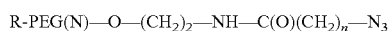
The following residues, 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581, are substituted with the following non-naturally encoded amino acid (hA; SEQ ID NO: 1):



The sequences utilized for site-specific incorporation of p-propargyl-tyrosine into hA are SEQ ID NO: 2 (hA), SEQ ID NO: 3 (muttRNA, *M. jannaschii* mtRNA_{CUA}^{Tyr}), and 8, 9 or 10 described in Example 2 above. The hA polypeptide containing the propargyl tyrosine is expressed in *E. coli* and purified using the conditions described in Example 3.

The purified hA containing propargyl-tyrosine dissolved at between 0.1-10 mg/mL in PB buffer (100 mM sodium phosphate, 0.15 M NaCl, pH=8) and a 10 to 1000-fold excess of an azide-containing PEG is added to the reaction mixture. A catalytic amount of CuSO₄ and Cu wire are then added to the reaction mixture. After the mixture is incubated (including but not limited to, about 4 hours at room temperature or 37° C., or overnight at 4° C.), H₂O is added and the mixture is filtered through a dialysis membrane. The sample can be analyzed for the addition, including but not limited to, by similar procedures described in Example 3.

In this Example, the PEG will have the following structure:



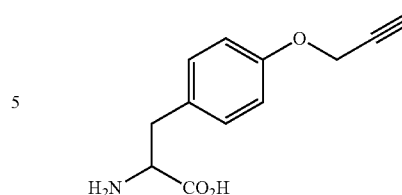
where R is methyl, n is 4 and N is 10,000 MW.

Example 8

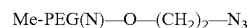
This example details substitution of a large, hydrophobic amino acid in a hA polypeptide with propargyl tyrosine.

A Phe, Trp or Tyr residue present within one the following positions of hA: 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581 (SEQ ID NO: 1), is substituted with the following non-naturally encoded amino acid as described in Example 7:

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Once modified, a PEG is attached to the hA polypeptide variant comprising the alkyne-containing amino acid. The PEG will have the following structure:

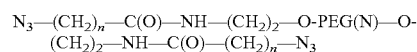


and coupling procedures would follow those in Example 7. This will generate a hA polypeptide variant comprising a non-naturally encoded amino acid that is approximately isosteric with one of the naturally-occurring, large hydrophobic amino acids and which is modified with a PEG derivative at a distinct site within the polypeptide.

Example 9

This example details generation of a hA polypeptide homodimer, heterodimer, homomultimer, or heteromultimer separated by one or more PEG linkers.

The alkyne-containing hA polypeptide variant produced in Example 7 is reacted with a bifunctional PEG derivative of the form:

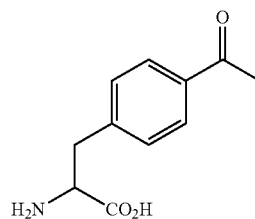


where n is 4 and the PEG has an average MW of approximately 5,000, to generate the corresponding hA polypeptide homodimer where the two hA molecules are physically separated by PEG. In an analogous manner a hA polypeptide may be coupled to one or more other polypeptides to form heterodimers, homomultimers, or heteromultimers. Coupling, purification, and analyses will be performed as in Examples 7 and 3.

Example 10

This example details coupling of a saccharide moiety to a hA polypeptide.

One residue of the following is substituted with the non-naturally encoded amino acid below: 17, 34, 55, 56, 58, 60, 81, 82, 86, 92, 94, 111, 114, 116, 119, 129, 170, 172, 173, 276, 277, 280, 297, 300, 301, 313, 317, 321, 362, 363, 364, 365, 368, 375, 397, 439, 442, 495, 496, 498, 500, 501, 505, 515, 538, 541, 542, 560, 562, 564, 574, 581 (hA, SEQ ID NO: 1) as described in Example 3.



Once modified, the hA polypeptide variant comprising the carbonyl-containing amino acid is reacted with a β -linked aminoxy analogue of N-acetylglucosamine (GlcNAc). The

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hA polypeptide variant (10 mg/mL) and the aminoxy saccharide (21 mM) are mixed in aqueous 100 mM sodium acetate buffer (pH 5.5) and incubated at 37° C. for 7 to 26 hours. A second saccharide is coupled to the first enzymatically by incubating the saccharide-conjugated hA polypeptide (5 mg/mL) with UDP-galactose (16 mM) and β -1,4-galactosyltransferase (0.4 units/mL) in 150 mM HEPES buffer (pH 7.4) for 48 hours at ambient temperature (Schanbacher et al. *J. Biol. Chem.* 1970, 245, 5057-5061).

Example 11

Generation of a hA Polypeptide Homodimer, Heterodimer, Homomultimer, or Heteromultimer in Which the Ha Molecules are Linked Directly

A hA polypeptide variant comprising the alkyne-containing amino acid can be directly coupled to another hA polypeptide variant comprising the azido-containing amino acid, each of which comprise non-naturally encoded amino acid substitutions at the sites described in, but not limited to, Example 10. This will generate the corresponding hA polypeptide homodimer where the two hA polypeptide variants are physically joined at the site II binding interface. In an analogous manner a hA polypeptide polypeptide may be coupled to one or more other polypeptides to form heterodimers, homomultimers, or heteromultimers. Coupling, purification, and analyses are performed as in Examples 3, 6, and 7.

Example 12

This example describes conjugations of hA comprising a non-naturally encoded amino acid with other biologically active molecules. The hA produced in Example 2 herein is reacted with a desired biologically active molecule such as a synthetic peptide, a small organic molecule, a polymer, a linker having one, two, three or more functional groups available for coupling to hA or other biologically active molecules, a protein or polypeptide other than hA, another hA molecule, or conjugation of a biologically active molecule to the non-natural amino acid and another biologically active molecule attached to the cysteine at position 34 of SEQ ID NO: 1. The desired biologically active molecule is reacted with the hA comprising a non-naturally encoded amino acid under conditions that allow covalent bond formation between the functional group of the non-naturally encoded amino acid of the hA with a complementary functional group on the biologically active molecule. The covalently bonded hA and desired biologically active molecule are further purified if desired utilizing the methods known in the art or described herein.

Example 13

This example details cloning and expression of a Fc with and without a non-naturally encoded amino acid in mammalian cells. [Cloning of the Fc DNA into expression vector, transformation of mammalian cells] SEQ ID NO: 20 shows the wild-type Fc polynucleotide sequence. This polynucleotide sequence encodes a human IgG1-Fc with a signal sequence that is absent in the purified protein. The codon underlined in this sequence was replaced by a selector codon, an amber codon, to obtain the mutant protein. The codon underlined encodes the aspartic acid (Asp; D) amino acid which is the first amino acid of the mature protein. SEQ ID NO: 21 shows the polypeptide sequence of the Fc with the signal sequence. SEQ ID NO: 22 shows the sequence of the

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mature Fc protein. SEQ ID NO: 23 shows the polynucleotide sequence encoding the mature Fc protein. See FIGS. 7A-D.

An introduced translation system that comprises an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS) is used to express Fc containing a non-naturally encoded amino acid. The O-RS preferentially aminoacylates the O-tRNA with a non-naturally encoded amino acid. In turn the translation system inserts the non-naturally encoded amino acid into Fc, in response to an encoded selector codon.

Transient Production of WT and D1pAF-Fc

CHO—S Freestyle™ cells (passage 10; Invitrogen, Carlsbad, Calif.) were seeded in 300 mL Freestyle™ CHO media (Invitrogen, Carlsbad, Calif.) at 5×10^5 cells/mL 24 hours prior to transfection. The transfection was conducted according to the manufacturer's instructions. Briefly, 375 mL Freestyle MAX™ reagent (Invitrogen, Carlsbad, Calif.) was incubated with plasmid encoding wild-type (WT) Fc (415 pg) or plasmids encoding an orthogonal tRNA (SEQ ID NO: 24), an orthogonal tRNA synthetase (5 μ g) (the encoding polynucleotide sequence shown as SEQ ID NO: 25) and Fc-D1_{TAG} (140 μ g) for 15 minutes. The non-naturally encoded amino acid will replace the aspartic acid (Asp; D) amino acid present at position 1 of the Fc sequence. The DNA transfection mix was added to 3.2×10^8 cells in a total of 300 mL. For cellular expression of protein from Fc-D1_{TAG}, para-acetylphenylalanine (pAF) was added to a final concentration of 1 mM. The cells were incubated at 34° C. at 8% CO₂ and 100 rpm. At 24 hours post-transfection, Select Phytone UF hydrolysate (Becton, Dickinson and Company, Franklin Lakes, N.J.) was added to a final concentration of 0.1%. The cultures were harvested at 72 hours post-transfection by centrifugation (10 minutes at 4,000 rpm), and the supernatants were filter sterilized using a 0.22 μ m filter. Purification of WT and D1pAF-Fc from CHO—S culture supernatants

Clarified culture supernatants were loaded onto a 5 mL HiTrap rProteinA FF pre-packed column (GE Healthcare, Piscataway, N.J.). The column was washed with 10 column volumes of PBS pH 7.4 prior to elution with 0.1M glycine pH 3.0. Fractions containing Fc were neutralized to approximately pH 7 with 0.03 volumes 0.5M Tris base. Fractions were pooled based on SDS-PAGE analysis, and the pool was concentrated with a 10,000 molecular weight cut off spin apparatus (Amicon) and dialyzed overnight against PBS pH 7.4+10% glycerol at 4° C. The Fc concentration was determined using absorbance at 280 nm. The extinction coefficient used for the Fc with para-acetylphenylalanine incorporation, D1pAF, was 1.35. The extinction coefficient used for WT Fc was 1.40. N-terminal sequencing and mass spectrometry demonstrated proper incorporation of pAF at the N-terminus of D1_{TAG}. This protein is referred to as D1pAF (Fc with pAF substituted at position 1).

Conjugation of 5K Amino-oxy PEG to D1pAF-Fc

Purified WT-Fc and D1pAF were buffer exchanged into conjugation buffer (20 mM sodium acetate, 20 g/L glycine, 5 g/L mannitol, 1 mM EDTA, pH 4.0) and concentrated to approximately 1.5 mg/mL. The samples were incubated in conjugation buffer alone or with 5K amino-oxy poly(ethylene)-glycol (PEG) at a final concentration of 15 g/L (50-fold molar excess over Fc monomer). Acetic hydrazide was added to all reactions at a final concentration of 50 mM to catalyze the conjugation reaction. Reactions were allowed to proceed at 28° C. for 48 hours. A 5 μ L aliquot was removed at 24 hours. Three μ g of each sample was analyzed by SDS PAGE. 4-12% bis-tris SDS-PAGE was performed under reducing and non-reducing conditions and coomassie stained. Reduced samples

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were separated using an MES buffer system, and non-reduced samples were separated with a MOPS buffer system.

FIG. 6 shows 5K PEG conjugation to the amino terminal pAF residue of human IgG1-Fc. Purified Fc (WT) and D1pAF-substituted Fc (D1pAF) were incubated in the presence (+) or absence (-) of 5K amino-oxy poly(ethylene)-glycol (PEG) for 24 or 48 hours at 28° C. Reduced (FIG. 6, Panel A) or non-reduced (FIG. 6, Panel B) samples were analyzed by coomassie blue staining of protein separated by SDS-PAGE.

FIG. 6, Panel A shows D1pAF+PEG exhibited a mass shift compared to D1pAF incubated without PEG (lanes 7 vs. 5, respectively). In contrast, no mass shift was observed after WT Fc was incubated with 5K PEG (lanes 3 and 6), demonstrating that the mass shift is pAF-dependent. SDS-PAGE analysis of non-reduced samples demonstrated that intact -Fc dimers were conjugated on one (PEG-D1pAF+D1pAF) or two (PEG-D1pAF+PEG-D1pAF) arms of the molecule (FIG. 6, Panel B). Staining intensity indicated that the majority of the material was doubly PEGylated Fc dimer (lane 7). The lower bands present in panel (FIG. 6, Panel B) are reduced forms of PEGylated and unPEGylated Fc monomer.

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As an illustrative, non-limiting example of the compositions, methods, techniques and strategies described herein, the description discussed adding macromolecular polymers to a Fc comprising a non-naturally encoded amino acid with the understanding that the compositions, methods, techniques and strategies described thereto are also applicable (with appropriate modifications, if necessary and for which one of skill in the art could make with the disclosures herein) to adding other functionalities, including but not limited to those listed above and/or to other Fc molecules.

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to those of ordinary skill in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, patent applications, and/or other documents cited in this application are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, and/or other document were individually indicated to be incorporated by reference for all purposes.

SEQ ID NO	SEQUENCE	Notes	
3	CCGCGCGGTAGTTCAGCAGGGCAGAACGGCGGACTCTAAATCCGCATGGC GCTGGTTCAAATCCGGCCCGCCGGACCA	<i>M. jannaschii</i> mtRNA ^{3'} CUA	tRNA
4	CCCAGGGTAG CCAAGCTCGG CCAACGGCGAC GGACTCTAA ATCCGTTCTC GTAGGAGTTC GAGGGTTCGA ATCCCTTCCC TGGGACCA	HLAD03; an optimized amber suppressor tRNA	tRNA
5	GCGAGGGTAG CCAAGCTCGG CCAACGGCGA CGGACTTCCT AATCCGTTCT CGTAGGAGTT CGAGGGTTCG AATCCCTCCC CTCGCACCA	HL325A; an optimized AGGA frameshift suppressor tRNA	tRNA
6	MDEFEMIKRNTSEIISEEELREVLKKDEKSAGIGFEPGSGKIFILGHYLQIKKMID LQNGEDILIIILLADLHAYLNQKGELDEIRKIGDYNKVFAMGLKAKYVYGS TFQLDKDYTLNVYRLALKTTLCRARRSMELIAREDENPKVAEVIYPIMQVNT YYLGVDDVAVGGMEQRKJEMLARELLPKVVCIHNPVLTGLDGEGKMSSS KGNFIAVDDSPREEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKF GGDLTVNSYEELESLEKNELHPMDLKNVAEELIKILEPIRIRCL	Aminoacyl tRNA synthetase for the incorporation of p- azido-L-phenylalanine p-Az-PheRS (6)	RS
7	MDEFEMIKRNTSEIESEEELREVLKKDEKSAGIGFEPGSGKIHLGHYLQIKKMID LQNGEDIELLADLHAYLNQKGELDEIRKIGDYNKVFAMGLKAKYVYGS SFQLDKDYTLNVYRLALKTTLCRARRSMELIAREDENPKVAEVIYPIMQVNT SWILGVDDVAVGGMEQRKITIMLARELLPKYVVCIHNPVLTGLDGEGKMSSS KGNFIAVDDSPREEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKF GGDLTVNSYEELESLEKNELHPMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- benzoyl-L- phenylalanine p-BpaRS(1)	RS
8	MDEFE MIKRN TSEII SEEEL REVLK KDEKS AAIGF EPSGK IHLGH YLQIK KMIDL QNAGF DIIIL LADLH AYLNQ KGELD EIRKI GDYNK KVFEA MGLKA KYVYG SPFQL DKDYT LNVYR LALKT TLKRA RRSME LIARE DENPK VAEVI YPIMQ VNAIY LAVID VAVGG MEQRK IHMLA RELLP KKVVC IHNPV LTGLD GEGKM SSSKG NFIIV DDSPE EIRAK IKKAY CPAGV VEGNP IMEIA KYFLE YPLTI KRPEK FGGDL TVNSY EELES LFPKNK ELHPM DLKNA VAEEL IKILE PIRKR L	Aminoacyl tRNA synthetase for the incorporation of propargyl- phenylalanine Propargyl-PheRS	RS
9	MDEFE MIKRN TSEII SEEEL REVLK KDEKS AAIGF EPSGK IHLGH YLQIK KMIDL QNAGF DIIIL LADLH AYLNQ KGELD EIRKI GDYNK KVFEA MGLKA KYVYG SPFQL DKDYT LNVYR LALKT TLKRA RRSME LIARE DENPK VAEVI YPIMQ VNIPY LPVID VAVGG MEQRK IHMLA RELLP KKVVC IHNPV LTGLD GEGKM SSSKG NFIIV DDSPE EIRAK IKKAY CPAGV VEGNP IMEIA KYFLE YPLTI KRPEK FGGDL TVNSY EELES LFPKNK ELHPM DLKNA VAEEL IKILE PIRKR L	Aminoacyl tRNA synthetase for the incorporation of propargyl phenylalanine Propargyl-PheRS	RS
10	MDEFE MIKRN TSEII SEEEL REVLK KDEKS AAIGF EPSGK IELGE YLQIK KMIDL QNAGF DIIIL LADLE AYLNQ KGELD EIRKI GDYNK KVFEA MGLKA KYVYG SKFQL DKDYT LNVYR LALKT TLKRA RRSME LIARE DENPK VAEVI YPIMQ VNAIY LAVID VAVGG MEQRK IHMLA RELLP KKVVC IHNPV LTGLD GEGKM SSSKG NFIIV DDSPE EIRAK IKKAY CPAGV VEGNP IMEIA KYFLE YPLTI KRPEK FGGDL TVNSY EELES LFPKNK ELHPM DLKNA VAEEL IKILE PIRKR L	Aminoacyl tRNA synthetase for the incorporation of propargyl- phenylalanine	RS

-continued

SEQ ID NO	SEQUENCE	Notes	
11	MDEFEMIKRNTSEIISEEELREVLKKDEKSATTGFEPSPOKIHLGHYLQIKKMID LQNAGEDHILLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGS NFQLDKDYTLNVYRLALKETLICRARRSMELIAREDENPKVAEVIYPIMQVN PLHYQGVDVAVGGMEQRKIIHMLARELLPKKVVCIHNPVLTGLDGEGKMSS SKGNFIAVDDSPPEIRAKIKKAYCPAGVVEGNPINIEIAKYFLEYPETIKRPEKE GGDLTVNSYEELESIEKNKELHPMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- azido-phenylalanine p-Az-PheRS (1)	RS
12	MDEFEMIKRNTSELISEEELREVLKKDEKSATIGFEPSPGKIHLGEYLQIKKMID LQNAGEDIELLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGS SFQWKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVNP LINQGVDDVAVGGMEQRKEHMLARELLPKKVVCIFINPVLTLGLDGEGKMSS KGNFIAVDDSPPEIRAKEKKAYCPAGVVEGNPIMEIAKYFLEYPETIKRPEKE GGDLTVNSYEELESFLKNKELHPIVIDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- azido-phenylalanine p-Az-PheRS (3)	RS
13	MDEFEMIKRNTSEIISEEELREVLKKDEKSALIGFEPSPGKIHLGHYLQIKKMID LQNAGEDIIILLADLI TAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGS TFQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVNP VHYQGVDV AVGGMEQRKIIHMLARELLPKICVVCITINPVLTLGLDGEGICMSSS KONFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKE GGDLTVNSYEEELSLEKNKELHEMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- azido-phenylalanine p-Az-PheRS (4)	RS
14	MDEFEMIKRNTSEIISEEELREVLKKDEKSATIGFEPSPGKIHLGHYLQIKKMID LQNAGFDITILLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGS SFQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVNP SHYQGVDVAVGGMEQRKIIHMLARELLPKKVVCIHNPVLTGLDGEGKMSSS KGNFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKF GGDLTVINISYEELESLEKNKELHEMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- azido-phenylalanine p-Az-PheRS (2)	RS
15	MDEFEMIKRNTSEIISEEELREVLKKDEKSALIGFEPSPGKIHLGHYLQIKKMID LQNAGFDIIILLADLI IAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGS EFQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVN GCHYRGVDVAVGGMEQRKEIMLARELLPKKYVCIHNPVLTGLDGEGKMSS SKGNFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKF GGDLTVNSYEELESFLKNKELHEMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- acetyl-phenylalanine (LW1)	RS
16	MDEFEMIKRNTSEISEEELREVLKKDEKSALIGFEPSPGKIHLHLYLQIKKMID LQNAGFDIIILLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGS EFQLDKDYTLNVYRLALKTTTLKARRSMELIAREDENPKVAEVIYPIMQVN GTHYRGVDVAVGGMBQRKIIHMLARELLPKKVVCIFINPVLTLGLDGEGMVISS SKGNHVAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKF GGDLIVNSYEEELSLEKNKELHEMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- acetyl phenylalanine (LW5)	RS
17	MDEFEMIKRNTSEIISEEELREVLKKDEKSAAGFEPSPGKIHLGHYLQIKKMID LQNAGEDIIILLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGS EFQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVN GGITYLGVDDVAVGGMEQRKIIHMLARELLPKKVVCIHNPVLTOLDGEGKMSSS KGNFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKE GGDLTVNSYEEELSFLKNKELHPMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- acetyl phenylalanine (LW6)	RS
18	MDEFEMIKRNTSEIISEEELREVLKKDEKSAAGFEPSPGKTFILGHYLQIKKMID LQNAGFDITLLADLI IAYLNQKGELDEIRKIGDYNKKVFEAMOLKAKYVYGS REQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVN VIHYDGVDDVAVGGMEQRKEHMLARELLPKKVVCIHNPVLTGLDGEGKMSS SKGNFAVDDSPPEIRAKIKKAYCPAGVVEGNRIMMAKYFLEYPLTIKRPEKF GGDLTVNSYEELESLEKNKELHPMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- azido-phenylalanine (AzPheRS-5)	RS
19	MDEFEMIKRNTSEIISEEELREVLKKDEKSAGIFEPSPGKIHLGHYLQIKKMID LQNAGEDIIILLADLHAYLNQKGELDEIRKIGDYNKKVFEAMOLKAKYVYGS TFQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVNT YYLGVDDVAVGGMEQRKIIHMLARELLPKKVVCIFINPVLTLGLDGEGKNISSS KGNFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLFYPLTIKRPEKF GODLTVNSYEELESLEKNKELHPMDLKNVAEELIKILEPIRKRL	Aminoacyl tRNA synthetase for the incorporation of p- azido-phenylalanine (AzPheRS-6)	RS

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 25

<210> SEQ ID NO 1

<211> LENGTH: 609

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 1

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Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1          5          10          15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
 20          25          30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
 35          40          45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
 50          55          60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
 65          70          75          80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
 85          90          95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
100          105          110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115          120          125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
130          135          140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145          150          155          160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165          170          175

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
180          185          190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
195          200          205

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
210          215          220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225          230          235          240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
245          250          255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
260          265          270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
275          280          285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
290          295          300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305          310          315          320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
325          330          335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
340          345          350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
355          360          365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
370          375          380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385          390          395          400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys

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405	410	415
Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu 420 425 430		
Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val 435 440 445		
Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His 450 455 460		
Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val 465 470 475 480		
Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg 485 490 495		
Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe 500 505 510		
Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala 515 520 525		
Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu 530 535 540		
Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys 545 550 555 560		
Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala 565 570 575		
Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe 580 585 590		
Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly 595 600 605		
Leu		

<210> SEQ ID NO 2

<211> LENGTH: 1830

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

```

atgaagtggg taacctttat ttcccttctt tttctcttta gctcggctta ttccaggggt    60
gtgtttcgtc gagatgcaca caagagtgag gttgctcadc ggtttaaaga ttggggagaa    120
gaaaatttca aagccttggg gttgattgcc tttgctcagt atcttcagca gtgtccattt    180
gaagatcatg taaaattagt gaatgaagta actgaatttg caaaaacatg tgttgctgat    240
gagtcagctg aaaatttgta caaatcactt catacccttt ttggagacaa attatgcaca    300
gttgcaactc ttcgtgaaac ctatggtgaa atggctgact gctgtgcaaa acaagaacct    360
gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattgggtg    420
agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttgaaa    480
aaatacttat atgaaattgc cagaagacat ccttactttt atgccccgga actccttttc    540
tttgctaaaa ggtataaagc tgcttttaca gaatgttgcc aagctgctga taaagctgcc    600
tgccctgttg caaagctcga tgaacttcgg gatgaaggga aggcttcgct tgccaaacag    660
agactcaagt gtgccagtct ccaaaaattt ggagaaagag ctttcaaagc atgggcagta    720
gctcgcctga gccagagatt tcccaaagct gagtttgag aagtttccaa gtttagtgaca    780
gatcttacca aagtcacac ggaatgctgc catggagatc tgettgaatg tgetgatgac    840
agggcggaac ttgccaagta tatctgtgaa aatcaagatt cgatctccag taaactgaag    900
gaatgctgtg aaaaacctct gttggaaaaa tccactgca ttgccgaagt ggaaatgat    960

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gagatgectg ctgacttgcc ttcattagct gctgattttg ttgaaagtaa ggatgtttgc 1020
aaaaactatg ctgaggcaaa ggatgtcttc ctgggcgatg ttttgatga atatgcaaga 1080
aggcatcctg attactctgt cgtgctgctg ctgagacttg ccaagacata tgaaccact 1140
ctagagaagt gctgtgcccg tgcagatcct catgaatgct atgccaaagt gttcgatgaa 1200
tttaaacctc ttgtggaaga gcctcagaat ttaatcaaac aaaattgtga gctttttgag 1260
cagcttgagg agtacaaatt ccagaatgcg ctattagttc gttacaccaa gaaagtaccc 1320
caagtgtcaa ctccaactct tgtagaggtc tcaagaaacc taggaaaagt gggcagcaaa 1380
tgttgtaaac atcctgaagc aaaaagaatg ccctgtgcag aagactatct atccgtggtc 1440
ctgaaccagt tatgtgtggt gcatgagaaa acgccagtaa gtgacagagt caccaaatgc 1500
tgcacagaat ccttggtgaa caggcgacca tgcttttcag ctctggaagt cgatgaaaca 1560
tacgttccca aagagtttaa tgctgaaaca ttcaccttcc atgcagatat atgcacactt 1620
tctgagaagg agagacaaat caagaacaaa actgcacttg ttgagctcgt gaaacacaag 1680
cccaaggcaa caaagagca actgaaagct gttatggatg atttcgcagc ttttgtagag 1740
aagtgtgca aggctgacga taaggagacc tgctttgccg aggagggtaa aaaacttgtt 1800
gctgcaagtc aagctgcctt aggcctataa 1830

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<210> SEQ ID NO 3
<211> LENGTH: 77
<212> TYPE: DNA
<213> ORGANISM: Methanococcus jannaschii

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<400> SEQUENCE: 3

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ccggcggtag ttcagcaggg cagaacggcg gactctaaat ccgcatggcg ctggttcaaa 60
tccggccccg cggaacca 77

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<210> SEQ ID NO 4
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: An optimized amber supressor tRNA

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<400> SEQUENCE: 4

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cccagggtag ccaagctcgg ccaacggcga cggactctaa atccgttctc gtaggagttc 60
gagggttcga atcccttccc tgggacca 88

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<210> SEQ ID NO 5
<211> LENGTH: 89
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: An optimized AGGA frameshift supressor tRNA

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<400> SEQUENCE: 5

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gcgagggtag ccaagctcgg ccaacggcga cggacttctt aatccgttct ctaggagtt 60
cgagggttcg aatccctccc ctgcacca 89

```

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<210> SEQ ID NO 6
<211> LENGTH: 306
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
of p-azido-L-phenylalanine

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<400> SEQUENCE: 6

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1 5 10 15
 Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Gly
 20 25 30
 Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
 35 40 45
 Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
 50 55 60
 Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
 65 70 75 80
 Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
 85 90 95
 Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Thr Phe Gln Leu Asp Lys
 100 105 110
 Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
 115 120 125
 Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
 130 135 140
 Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Thr Tyr Tyr
 145 150 155 160
 Tyr Leu Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile
 165 170 175
 His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
 180 185 190
 Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
 195 200 205
 Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
 210 215 220
 Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
 225 230 235 240
 Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
 245 250 255
 Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
 260 265 270
 Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
 275 280 285
 Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
 290 295 300
 Arg Leu
 305

<210> SEQ ID NO 7

<211> LENGTH: 305

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
 of p-benzoyl-L-phenylalanine

<400> SEQUENCE: 7

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1 5 10 15
 Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Ala
 20 25 30

-continued

Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
 35 40 45
 Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
 50 55 60
 Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
 65 70 75 80
 Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
 85 90 95
 Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Pro Phe Gln Leu Asp Lys
 100 105 110
 Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
 115 120 125
 Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
 130 135 140
 Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Ala Ile Tyr
 145 150 155 160
 Leu Ala Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile His
 165 170 175
 Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His Asn
 180 185 190
 Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser Lys
 195 200 205
 Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala Lys
 210 215 220
 Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro Ile
 225 230 235 240
 Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys Arg
 245 250 255
 Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu Leu
 260 265 270
 Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys Asn
 275 280 285
 Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys Arg
 290 295 300
 Leu
 305

<210> SEQ ID NO 8
 <211> LENGTH: 305
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
 of propargyl-phenylalanine

<400> SEQUENCE: 8

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1 5 10 15
 Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Ala
 20 25 30
 Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
 35 40 45
 Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
 50 55 60
 Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp

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65	70	75	80
Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met	85	90	95
Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Pro Phe Gln Leu Asp Lys	100	105	110
Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys	115	120	125
Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro	130	135	140
Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Ala Ile Tyr	145	150	155
Leu Ala Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile His	165	170	175
Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His Asn	180	185	190
Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser Lys	195	200	205
Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala Lys	210	215	220
Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro Ile	225	230	235
Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys Arg	245	250	255
Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu Leu	260	265	270
Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys Asn	275	280	285
Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys Arg	290	295	300
Leu			
305			

<210> SEQ ID NO 9

<211> LENGTH: 305

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
of propargyl-phenylalanine

<400> SEQUENCE: 9

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser	1	5	10	15
Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Ala	20	25	30	
Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln	35	40	45	
Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile	50	55	60	
Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp	65	70	75	80
Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met	85	90	95	
Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Pro Phe Gln Leu Asp Lys	100	105	110	

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Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
   115                               120                               125

Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
   130                               135                               140

Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Ile Pro Tyr
   145                               150                               155                               160

Leu Pro Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile His
   165                               170                               175

Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His Asn
   180                               185                               190

Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser Lys
   195                               200                               205

Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala Lys
   210                               215                               220

Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro Ile
   225                               230                               235                               240

Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys Arg
   245                               250                               255

Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu Leu
   260                               265                               270

Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys Asn
   275                               280                               285

Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys Arg
   290                               295                               300

Leu
305

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<210> SEQ ID NO 10
<211> LENGTH: 305
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
      of propargyl-phenylalanine

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<400> SEQUENCE: 10

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Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1      5      10      15

Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Ala
 20     25     30

Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
 35     40     45

Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
 50     55     60

Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
 65     70     75     80

Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
 85     90     95

Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Lys Phe Gln Leu Asp Lys
100    105    110

Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
115    120    125

Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
130    135    140

Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Ala Ile Tyr
145    150    155    160

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195	200	205
Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala		
210	215	220
Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro		
225	230	235 240
Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys		
	245	250 255
Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu		
	260	265 270
Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys		
	275	280 285
Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys		
	290	295 300
Arg Leu		
305		

<210> SEQ ID NO 12

<211> LENGTH: 306

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
of p-azido-phenylalanine

<400> SEQUENCE: 12

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser		
1	5	10 15
Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Thr		
	20	25 30
Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln		
	35	40 45
Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile		
	50	55 60
Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp		
	65	70 75 80
Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met		
	85	90 95
Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Ser Phe Gln Leu Asp Lys		
	100	105 110
Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys		
	115	120 125
Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro		
	130	135 140
Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Pro Leu His		
	145	150 155 160
Tyr Gln Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile		
	165	170 175
His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His		
	180	185 190
Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser		
	195	200 205
Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala		
	210	215 220
Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro		
	225	230 235 240

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Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
      245                      250                      255

Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
      260                      265                      270

Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
      275                      280                      285

Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
      290                      295                      300

Arg Leu
305

```

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<210> SEQ ID NO 13
<211> LENGTH: 306
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
      of p-azido-phenylalanine

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<400> SEQUENCE: 13

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```

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
1      5      10      15

Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Leu
20     25     30

Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
35     40     45

Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
50     55     60

Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
65     70     75     80

Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
85     90     95

Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Thr Phe Gln Leu Asp Lys
100    105    110

Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
115    120    125

Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
130    135    140

Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Pro Val His
145    150    155    160

Tyr Gln Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile
165    170    175

His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
180    185    190

Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
195    200    205

Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
210    215    220

Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
225    230    235    240

Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
245    250    255

Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
260    265    270

Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
275    280    285

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Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
 290 295 300

Arg Leu
 305

<210> SEQ ID NO 14
 <211> LENGTH: 306
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
 of p-azido-phenylalanine

<400> SEQUENCE: 14

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1 5 10 15

Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Thr
 20 25 30

Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
 35 40 45

Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
 50 55 60

Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
 65 70 75 80

Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
 85 90 95

Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Ser Phe Gln Leu Asp Lys
 100 105 110

Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
 115 120 125

Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
 130 135 140

Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Pro Ser His
 145 150 155 160

Tyr Gln Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile
 165 170 175

His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
 180 185 190

Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
 195 200 205

Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
 210 215 220

Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
 225 230 235 240

Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
 245 250 255

Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
 260 265 270

Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
 275 280 285

Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
 290 295 300

Arg Leu
 305

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<210> SEQ ID NO 15
<211> LENGTH: 306
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
      of p-acetyl-phenylalanine

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<400> SEQUENCE: 15

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```

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1             5             10             15

Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Leu
      20             25             30

Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
      35             40             45

Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
      50             55             60

Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
      65             70             75             80

Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
      85             90             95

Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Glu Phe Gln Leu Asp Lys
      100            105            110

Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
      115            120            125

Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
      130            135            140

Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Gly Cys His
      145            150            155            160

Tyr Arg Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile
      165            170            175

His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
      180            185            190

Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
      195            200            205

Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
      210            215            220

Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
      225            230            235            240

Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
      245            250            255

Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
      260            265            270

Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
      275            280            285

Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
      290            295            300

Arg Leu
305

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<210> SEQ ID NO 16
<211> LENGTH: 306
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
      of p-acetyl-phenylalanine

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<400> SEQUENCE: 16

```

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
1           5           10           15
Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Leu
20           25           30
Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
35           40           45
Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
50           55           60
Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
65           70           75           80
Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
85           90           95
Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Glu Phe Gln Leu Asp Lys
100          105          110
Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
115          120          125
Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
130          135          140
Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Gly Thr His
145          150          155          160
Tyr Arg Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile
165          170          175
His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
180          185          190
Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
195          200          205
Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
210          215          220
Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
225          230          235          240
Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
245          250          255
Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
260          265          270
Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
275          280          285
Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
290          295          300
Arg Leu
305

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<210> SEQ ID NO 17

<211> LENGTH: 306

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
of p-acetyl-phenylalanine

<400> SEQUENCE: 17

```

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
1           5           10           15
Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Ala
20           25           30

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Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
   35                               40               45

Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
   50                               55               60

Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
   65                               70               75               80

Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
   85                               90               95

Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Glu Phe Gln Leu Asp Lys
  100                               105              110

Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
  115                               120              125

Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
  130                               135              140

Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Gly Gly His
  145                               150              155              160

Tyr Leu Gly Val Asp Val Ile Val Gly Gly Met Glu Gln Arg Lys Ile
  165                               170              175

His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
  180                               185              190

Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
  195                               200              205

Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
  210                               215              220

Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
  225                               230              235              240

Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
  245                               250              255

Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
  260                               265              270

Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
  275                               280              285

Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
  290                               295              300

Arg Leu
305

```

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<210> SEQ ID NO 18
<211> LENGTH: 306
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
      of p-azido-phenylalanine

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<400> SEQUENCE: 18

```

```

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1           5           10           15

Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Ala
 20           25           30

Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
 35           40           45

Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
 50           55           60

Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
 65           70           75           80

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Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
 85 90 95
 Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Arg Phe Gln Leu Asp Lys
 100 105 110
 Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys
 115 120 125
 Arg Ala Arg Arg Ser Met Glu Leu Ile Ala Arg Glu Asp Glu Asn Pro
 130 135 140
 Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Val Ile His
 145 150 155 160
 Tyr Asp Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile
 165 170 175
 His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His
 180 185 190
 Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser
 195 200 205
 Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala
 210 215 220
 Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro
 225 230 235 240
 Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys
 245 250 255
 Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu
 260 265 270
 Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys
 275 280 285
 Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys
 290 295 300
 Arg Leu
 305

<210> SEQ ID NO 19
 <211> LENGTH: 306
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Aminoacyl tRNA synthetase for the incorporation
 of p-azido-phenylalanine

<400> SEQUENCE: 19

Met Asp Glu Phe Glu Met Ile Lys Arg Asn Thr Ser Glu Ile Ile Ser
 1 5 10 15
 Glu Glu Glu Leu Arg Glu Val Leu Lys Lys Asp Glu Lys Ser Ala Gly
 20 25 30
 Ile Gly Phe Glu Pro Ser Gly Lys Ile His Leu Gly His Tyr Leu Gln
 35 40 45
 Ile Lys Lys Met Ile Asp Leu Gln Asn Ala Gly Phe Asp Ile Ile Ile
 50 55 60
 Leu Leu Ala Asp Leu His Ala Tyr Leu Asn Gln Lys Gly Glu Leu Asp
 65 70 75 80
 Glu Ile Arg Lys Ile Gly Asp Tyr Asn Lys Lys Val Phe Glu Ala Met
 85 90 95
 Gly Leu Lys Ala Lys Tyr Val Tyr Gly Ser Thr Phe Gln Leu Asp Lys
 100 105 110
 Asp Tyr Thr Leu Asn Val Tyr Arg Leu Ala Leu Lys Thr Thr Leu Lys

-continued

115	120	125
Arg Ala Arg Arg Ser Met	Glu Leu Ile Ala Arg	Glu Asp Glu Asn Pro
130	135	140
Lys Val Ala Glu Val Ile Tyr Pro Ile Met Gln Val Asn Thr Tyr Tyr		
145	150	155 160
Tyr Leu Gly Val Asp Val Ala Val Gly Gly Met Glu Gln Arg Lys Ile		
165	170	175
His Met Leu Ala Arg Glu Leu Leu Pro Lys Lys Val Val Cys Ile His		
180	185	190
Asn Pro Val Leu Thr Gly Leu Asp Gly Glu Gly Lys Met Ser Ser Ser		
195	200	205
Lys Gly Asn Phe Ile Ala Val Asp Asp Ser Pro Glu Glu Ile Arg Ala		
210	215	220
Lys Ile Lys Lys Ala Tyr Cys Pro Ala Gly Val Val Glu Gly Asn Pro		
225	230	235 240
Ile Met Glu Ile Ala Lys Tyr Phe Leu Glu Tyr Pro Leu Thr Ile Lys		
245	250	255
Arg Pro Glu Lys Phe Gly Gly Asp Leu Thr Val Asn Ser Tyr Glu Glu		
260	265	270
Leu Glu Ser Leu Phe Lys Asn Lys Glu Leu His Pro Met Asp Leu Lys		
275	280	285
Asn Ala Val Ala Glu Glu Leu Ile Lys Ile Leu Glu Pro Ile Arg Lys		
290	295	300
Arg Leu		
305		

<210> SEQ ID NO 20

<211> LENGTH: 744

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

```

atgtacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacgaattcg      60
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc      120
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca      180
tgcggtggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac      240
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac      300
cgtgtgtgta gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag      360
tgcaagggtc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa      420
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag      480
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag      540
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctccccgt gctggactcc      600
gacggctcct tcttctctta cagcaagctc accgtggaca agagcagggt gcagcagggg      660
aacgtcttct catgctccgt gatgcacgag gctctgcaca accactacac gcagaagagc      720
ctctccctgt ctccgggtaa atga                                             744

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<210> SEQ ID NO 21

<211> LENGTH: 247

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

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```

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1           5           10           15

Val Thr Asn Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
          20           25           30

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
          35           40           45

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
          50           55           60

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
          65           70           75           80

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
          85           90           95

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
          100          105          110

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
          115          120          125

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
          130          135          140

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
          145          150          155          160

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
          165          170          175

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
          180          185          190

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
          195          200          205

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
          210          215          220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
          225          230          235          240

Leu Ser Leu Ser Pro Gly Lys
          245

```

<210> SEQ ID NO 22

<211> LENGTH: 227

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

```

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1           5           10           15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
          20           25           30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
          35           40           45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
          50           55           60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
          65           70           75           80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
          85           90           95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
          100          105          110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

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115	120	125	
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser			
130	135	140	
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu			
145	150	155	160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro			
	165	170	175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val			
	180	185	190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met			
	195	200	205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser			
	210	215	220
Pro Gly Lys			
225			
<210> SEQ ID NO 23			
<211> LENGTH: 684			
<212> TYPE: DNA			
<213> ORGANISM: Homo sapiens			
<400> SEQUENCE: 23			
gacaaaaactc acacatgccc accgtgcccc gcacctgaac tcctgggggg accgtcagtc			60
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca			120
tgctgtgtgg tggacgtgag ccacgaagac cctgaggtea agttcaactg gtacgtggac			180
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac			240
cgtgtgtgta cgcctctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag			300
tgcaagggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa			360
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag			420
aaccaggtea gcctgacctg cctggtaaaa ggctttctatc ccagcgacat cgccgtggag			480
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccggt gctggactcc			540
gacggctcct tcttctctta cagcaagctc accgtggaca agagcagggtg gcagcagggg			600
aacgtcttct catgctccgt gatgcacgag gctctgcaca accactacac gcagaagagc			660
ctctccctgt ctccgggtaa atga			684
<210> SEQ ID NO 24			
<211> LENGTH: 82			
<212> TYPE: DNA			
<213> ORGANISM: Homo sapiens			
<400> SEQUENCE: 24			
ggtggggtag cgaagtggct aaacgcggcg gactctaaat ccgctccctt tgggttcggc			60
ggttcgaatc cgtccccac ca			82
<210> SEQ ID NO 25			
<211> LENGTH: 1299			
<212> TYPE: DNA			
<213> ORGANISM: Homo sapiens			
<400> SEQUENCE: 25			
atggcaagca gtaacttgat taaacaattg caagagcggg ggctggtagc ccaggtgacg			60
gacgaggaag cgttagcaga gcgactggcg caaggcccg tgcgctcat ttgcggcttc			120

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gacctaaccg	ctgacagett	gcatttgggg	catcttggtc	cattgttatg	cctgaaacgc	180
ttccagcagg	cgggccacaa	gccggttgcg	ctggtaggcg	gcgcgacggg	tctgattggc	240
gaccgcagct	tcaaagctgc	cgagcgtaag	ctgaacacgc	aagaaactgt	tcaggagtgg	300
gtggacaaaa	tccgtaagca	ggttgccccg	ttcctcgatt	tcgactgtgg	agaaaaactct	360
gctatcgctg	cgaacaacta	tgactgggtc	ggcaatatga	atgtgctgac	cttcctgcgc	420
gatattggca	aacactttct	cgtaaccag	atgatcaaca	aagaagcggg	taagcagcgt	480
ctcaaccgtg	aaggctcagg	gatttcgttc	actgagtttt	cctacaacct	gttgagggtt	540
tatggtatgg	cctgtgctaa	caaacagtac	ggtgtgggtc	tgcaaatgg	tggttctgac	600
cagtggtgta	acatcacttc	tggtatcgac	ctgacccgtc	gtctgcatca	gaatcagggt	660
tttgccctga	ccgttccgct	gatcactaaa	gcagatggca	ccaaatttgg	taaaactgaa	720
ggcggcgctg	tctggttgga	tccgaagaaa	accagcccg	acaaattcta	ccagttctgg	780
atcaacactg	cggatgcca	cgtttaccgc	ttcctgaagt	tcttcacctt	tatgagcatt	840
gaagagatca	acgccctgga	agaagaagat	aaaaacagcg	gtaaagcacc	gcgcgcccag	900
tatgtactgg	cggagcaggt	gactcgtctg	gttcacgggt	aagaagggtt	acaggcgcca	960
aaacgtatta	ccgaatgctt	gttcagcgg	tctttgagtg	cgctgagtga	agcggacttc	1020
gaacagctgg	cgcaggacgg	cgtaccgatg	gttgagatgg	aaaaggcgcg	agacctgatg	1080
caggcactgg	tcgattctga	actgcaacct	tcccgtggtc	aggcacgtaa	aactatcgcc	1140
tccaatgcca	tcaccattaa	cgttgaaaaa	cagtcggatc	ctgaatactt	ctttaagaa	1200
gaagatcgtc	tgtttggtcg	ttttacctta	ctgcgtcgcg	gtaaaaagaa	ttactgtctg	1260
atgtgctgga	aagattataa	agatgatgac	gacaaataa			1299

What is claimed is:

1. A human serum albumin (HSA) comprising a non-naturally encoded amino acid at one or more of the following positions: 34, 82, 172, 301, 364, and 505 of SEQ ID NO: 1, linked to one or more biologically active molecules selected from the group consisting of relaxin, angiotensin peptides, antibiotic peptides, antigenic polypeptides, anti-microbial peptides, apoptosis related peptides, atrial natriuretic peptides, bag cell peptides, bombesin peptides, bone GLA peptides, bradykinin peptides, brain natriuretic peptides, C-peptides, C-type natriuretic peptides, calcitonin peptides, calcitonin gene related peptides, CART peptides, casomorphin peptides, chemotactic peptides, cholecystokinin pep-

tides, colony-stimulating factor peptides, corticotropin releasing factor peptides, cortistatin peptides, cytokine peptides, dermorphin peptides, dynorphin peptides, endorphin peptides, endothelin peptides, ETa receptor antagonist peptides, or ETb receptor antagonist peptides.

2. The HSA of claim 1, wherein the non-naturally encoded amino acid is para-acetylphenylalanine.

3. The HSA of claim 1, wherein the non-naturally encoded amino acid is para-azido-phenylalanine.

4. The HSA of claim 1, wherein the non-naturally encoded amino acid is para-amino-phenylalanine.

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